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(54) Title: NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

(57) Abstract: Nucleotide sequences are isolated from *Arabidopsis thaliana* that code for proteins essential for plant growth and development. The essentially of the proteins may be exploited by recombinantly expressing the proteins and using them in screening assays to identify compounds that interact with or inhibit the proteins and are therefore potential herbicides.

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## NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

The present invention pertains to nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. The invention particularly relates to methods of using these proteins as herbicide targets, based on this essentiality.

The use of herbicides to control undesirable vegetation such as weeds in crop fields has become almost a universal practice. The herbicide market exceeds 15 billion dollars annually. Despite this extensive use, weed control remains a significant and costly problem for farmers.

Effective use of herbicides requires sound management. For instance, the time and method of application and stage of weed plant development are critical to achieving good weed control with herbicides. Because various weed species are resistant to herbicides, the production of effective new herbicides becomes increasingly important. New herbicides can now be discovered using high-throughput screens that implement recombinant DNA technology. Metabolic enzymes found to be essential to plant growth and development can be recombinantly produced through standard molecular biological techniques and utilized as herbicide targets in screens for novel inhibitors of the enzyme activity. More generally, any essential plant protein can be used to screen for inhibitors of its activity. The novel inhibitors discovered through such screens may then be used as herbicides to control undesirable vegetation.

In view of the above, there remain persistent and ongoing problems with unwanted or detrimental vegetation growth (*e.g.* weeds). Furthermore, as the population continues to grow, there will be increasing food shortages. Therefore, there exists a long felt, yet unfulfilled need, to find new, effective, and economic herbicides.

In view of these needs, it is an object of the invention to provide nucleic acid molecules from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. It is another object to provide the essential proteins encoded by these essential nucleotide sequences for assay development to identify

inhibitory compounds with herbicidal activity. It is still another object of the present invention to provide an effective and beneficial method for identifying new or improved herbicides using the essential proteins of the invention.

In furtherance of these and other objects, the present invention provides nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant viability. Genetic results show that when any of the nucleotide sequences of the invention are mutated in *Arabidopsis thaliana*, the resulting phenotype is embryo or seedling lethal in the homozygous state. In particular, by using *Ac/Ds* transposon or T-DNA-mediated mutagenesis, the inventors of the present invention are the first to demonstrate that the activity of each protein of the present invention is essential for plant growth in *Arabidopsis thaliana*.

This knowledge is exploited to provide novel herbicide modes of action. The critical role in plant growth of the proteins encoded by each of the nucleotide sequences of the invention implies that chemicals that inhibit the function of any one of these proteins in plants are likely to have detrimental effects on plants and are potentially good herbicide candidates. Thus, the proteins encoded by the essential nucleotide sequences provide the bases for assays designed to easily and rapidly identify novel herbicides.

The present invention therefore provides methods of using a purified protein encoded by any one of the nucleotide sequences described below to identify inhibitors thereof, which can then be used as herbicides to suppress the growth of undesirable vegetation, *e.g.* in fields where crops are grown, particularly agronomically important crops such as maize and other cereal crops such as wheat, oats, rye, sorghum, rice, barley, millet, turf and forage grasses, and the like, as well as cotton, sugar cane, sugar beet, oilseed rape, and soybeans.

Disclosed herein are nucleic acid molecules isolated from *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence, the complement of which hybridizes under stringent conditions to a sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-95. In another embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

The present invention also provides a chimeric construct comprising a promoter operatively linked to a nucleic acid molecule according to the present invention, wherein the promoter is preferably functional in a eukaryote, wherein the promoter is preferably heterologous to the nucleic acid molecule. The present invention further provides a recombina-  
5 nt vector comprising a chimeric construct according to the present invention, wherein said vector is capable of being stably transformed into a host cell. The present invention still further provides a host cell comprising a nucleic acid molecule according to the present invention, wherein said nucleic acid molecule is preferably expressible in the cell. The host cell is preferably selected from the group consisting of a plant cell, a yeast cell, an insect cell, and a prokaryotic cell. The present invention additionally provides a plant or seed  
10 comprising a plant cell according to the present invention.

The present invention also provides proteins essential for plant growth in *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more  
15 preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. In accordance with another embodiment, the present invention also relates to the recombinant production of proteins of the invention and methods of using the proteins of the invention in assays for identifying compounds that interact with the protein.

According to another aspect, the present invention provides a method of identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid  
20 sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind to said polypeptide, under conditions conducive to binding; (b) selecting a compound identified in (a) that binds to said polypeptide; (c) applying a compound selected in (b) to a  
25 plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid  
30 sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID



NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

According to yet another aspect, the present invention provides a method of  
5 identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit the activity of said polypeptide, under conditions conducive to inhibition; (b) selecting a compound identified in (a) that inhibits the activity of said polypeptide; (c)  
10 applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid sequence at least 99% identical to an amino acid  
15 sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

20 The present invention still further provides a method for killing or inhibiting the growth or viability of a plant, comprising inhibiting expression in said plant of a protein having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

25 Other objects and advantages of the present invention will become apparent to those skilled in the art and from a study of the following description of the invention and non-limiting examples. The entire contents of all publications mentioned herein are hereby incorporated by reference.

#### 30 BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

Odd numbered SEQ ID NOs:1-95 are nucleotide sequences isolated from *Arabidopsis thaliana* that are more fully described in Table 5 below.

Even numbered SEQ ID NOs:2-96 are protein sequences encoded by the immediately preceding nucleotide sequence, *e.g.*, SEQ ID NO:2 is the protein encoded by the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:4 is the protein encoded by the nucleotide sequence of SEQ ID NO:3, etc.

5           SEQ ID NOs:101-125 are PCR primers.

## DEFINITIONS

For clarity, certain terms used in the specification are defined and presented as follows:

10           “Associated with / operatively linked” refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

15           A “chimeric construct” is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulatory nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulatory nucleic acid sequence of the chimeric construct is not normally  
20           operatively linked to the associated nucleic acid sequence as found in nature.

Co-factor: natural reactant, such as an organic molecule or a metal ion, required in an enzyme-catalyzed reaction. A co-factor is *e.g.* NAD(P), riboflavin (including FAD and FMN), folate, molybdopterin, thiamin, biotin, lipoic acid, pantothenic acid and coenzyme A, S-adenosylmethionine, pyridoxal phosphate, ubiquinone, menaquinone. Optionally, a co-factor  
25           can be regenerated and reused.

A “coding sequence” is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

Complementary: “complementary” refers to two nucleotide sequences that comprise  
30           antiparallel nucleotide sequences capable of pairing with one another upon formation of hydrogen bonds between the complementary base residues in the antiparallel nucleotide sequences.

Enzyme activity: means herein the ability of an enzyme to catalyze the conversion of a substrate into a product. A substrate for the enzyme comprises the natural substrate of the enzyme but also comprises analogues of the natural substrate, which can also be converted, by the enzyme into a product or into an analogue of a product. The activity of the enzyme is measured for example by determining the amount of product in the reaction after a certain period of time, or by determining the amount of substrate remaining in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of an unused co-factor of the reaction remaining in the reaction mixture after a certain period of time or by determining the amount of used co-factor in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of a donor of free energy or energy-rich molecule (*e.g.* ATP, phosphoenolpyruvate, acetyl phosphate or phosphocreatine) remaining in the reaction mixture after a certain period of time or by determining the amount of a used donor of free energy or energy-rich molecule (*e.g.* ADP, pyruvate, acetate or creatine) in the reaction mixture after a certain period of time.

Essential: an "essential" *Arabidopsis thaliana* nucleotide sequence is a nucleotide sequence encoding a protein such as *e.g.* a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein that is essential to the growth or survival of the plant.

Expression Cassette: "Expression cassette" as used herein means a nucleic acid molecule capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operatively linked to the nucleotide sequence of interest which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, *i.e.*, the particular DNA sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of

the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter that initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as a plant, the promoter can also be specific to a particular tissue or organ or stage of

5 development.

Gene: the term "gene" is used broadly to refer to any segment of DNA associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety  
10 of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

Heterologous/exogenous: The terms "heterologous" and "exogenous" when used herein to refer to a nucleic acid sequence (*e.g.* a DNA sequence) or a gene, refer to a sequence  
15 that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or  
20 heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" nucleic acid (*e.g.* DNA) sequence is a nucleic acid (*e.g.* DNA) sequence naturally associated with a host cell into which it is introduced.

25 Hybridization: The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular DNA or RNA). "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be  
30 accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

Inhibitor: a chemical substance that inactivates the enzymatic activity of a protein such as a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein. The term "herbicide" (or "herbicidal compound") is used herein to define an inhibitor applied to a plant at any stage of development, whereby the herbicide inhibits the growth of the plant or kills the plant.

Interaction: quality or state of mutual action such that the effectiveness or toxicity of one protein or compound on another protein is inhibitory (antagonists) or enhancing (agonists).

A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

Isogenic: plants that are genetically identical, except that they may differ by the presence or absence of a heterologous DNA sequence.

Isolated: in the context of the present invention, an isolated DNA molecule or an isolated enzyme is a DNA molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, in a transgenic host cell.

Mature protein: protein from which the transit peptide, signal peptide, and/or propeptide portions have been removed.

Minimal Promoter: the smallest piece of a promoter, such as a TATA element, that can support any transcription. A minimal promoter typically has greatly reduced promoter activity in the absence of upstream activation. In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription.

Modified Enzyme Activity: enzyme activity different from that which naturally occurs in a plant (*i.e.* enzyme activity that occurs naturally in the absence of direct or indirect manipulation of such activity by man), which is tolerant to inhibitors that inhibit the naturally occurring enzyme activity.

Native: refers to a gene that is present in the genome of an untransformed plant cell.

Naturally occurring: the term "naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be

isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

Nucleic acid: the term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.* degenerate codon substitutions) and complementary sequences and as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.* 19: 5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260: 2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8: 91-98 (1994)). The terms "nucleic acid" or "nucleic acid sequence" may also be used interchangeably with gene, cDNA, and mRNA encoded by a gene.

"ORF" means open reading frame.

Percent identity: the phrases "percent identical" or "percent identical," in the context of two nucleic acid or protein sequences, refers to two or more sequences or subsequences that have for example 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably at least 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Preferably, the percent identity exists over a region of the sequences that is at least about 50 residues in length, more preferably over a region of at least about 100 residues, and most preferably the percent identity exists over at least about 150 residues. In an especially preferred embodiment, the percent identity exists over the entire length of the coding regions.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2: 482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48: 443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85: 2444 (1988), by  
5 computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally*, Ausubel *et al.*, *infra*).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol.*  
10 *Biol.* 215: 403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database  
15 sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching  
20 residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either  
25 sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see*  
30 Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin &

Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Pre-protein: protein that is normally targeted to a cellular organelle, such as a chloroplast, and still comprises its native transit peptide.

Purified: the term "purified," when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the natural state. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or protein is at least about 50% pure, more preferably at least about 85% pure, and most preferably at least about 99% pure.

Two nucleic acids are "recombined" when sequences from each of the two nucleic acids are combined in a progeny nucleic acid. Two sequences are "directly" recombined when both of the nucleic acids are substrates for recombination. Two sequences are "indirectly recombined" when the sequences are recombined using an intermediate such as a cross-over oligonucleotide. For indirect recombination, no more than one of the sequences is an actual substrate for recombination, and in some cases, neither sequence is a substrate for recombination.

"Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operatively linked to the nucleotide sequence of interest and termination signals. They also typically encompass sequences required for proper translation of the nucleotide sequence.

Significant Increase: an increase in enzymatic activity that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater



of the activity of the wild-type enzyme in the presence of the inhibitor, more preferably an increase by about 5-fold or greater, and most preferably an increase by about 10-fold or greater.

Significantly less: means that the amount of a product of an enzymatic reaction is  
5 reduced by more than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater of the activity of the wild-type enzyme in the absence of the inhibitor, more preferably an decrease by about 5-fold or greater, and most preferably an decrease by about 10-fold or greater.

Specific Binding/Immunological Cross-Reactivity: An indication that two nucleic  
10 acid sequences or proteins are substantially identical is that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, a protein is typically substantially identical to a second protein, for example, where the two proteins differ only by conservative substitutions. The phrase "specifically (or selectively) binds to an antibody," or "specifically (or selectively)  
15 immunoreactive with," when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions  
20 may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to the protein with the amino acid sequence encoded by any of the nucleic acid sequences of the invention can be selected to obtain antibodies specifically immunoreactive with that protein and not with other proteins except for polymorphic variants. A variety of immunoassay formats may be used to select antibodies specifically  
25 immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays, Western blots, or immunohistochemistry are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York "Harlow and Lane"), for a description of immunoassay formats and conditions that can be used to determine specific  
30 immunoreactivity. Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. An extensive  
5 guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes* part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at  
10 a defined ionic strength and pH. Typically, under "stringent conditions" a probe will hybridize to its target subsequence, but to no other sequences.

The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the  $T_m$  for a particular probe. An example of stringent hybridization  
15 conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (*see*, Sambrook, *infra*,  
20 for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 4-6x SSC at 40°C for 15 minutes. For short probes (*e.g.*, about 10 to 50 nucleotides), stringent conditions  
25 typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a  
30 specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially

identical. This occurs, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone nucleotide sequences that are homologues of reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference  
5 nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA  
10 at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

A "subsequence" refers to a sequence of nucleic acids or amino acids that comprise a  
15 part of a longer sequence of nucleic acids or amino acids (*e.g.*, protein) respectively.

Substrate: a substrate is the molecule that an enzyme naturally recognizes and converts to a product in the biochemical pathway in which the enzyme naturally carries out its function, or is a modified version of the molecule, which is also recognized by the enzyme and is converted by the enzyme to a product in an enzymatic reaction similar to the naturally-  
20 occurring reaction.

Transformation: a process for introducing heterologous DNA into a plant cell, plant tissue, or plant. Transformed plant cells, plant tissue, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a  
25 bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also  
30 transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, *e.g.*, a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

Viability: "viability" as used herein refers to a fitness parameter of a plant. Plants are assayed for their homozygous performance of plant development, indicating which proteins are essential for plant growth.

5 I. Identification of Essential *Arabidopsis thaliana* Nucleotide Sequences and Encoded Proteins Using *Ac/Ds* Transposon or T-DNA-Mediated Mutagenesis

As shown in the examples below, the essentiality of the nucleotide sequences described herein for normal plant growth and development, have been demonstrated for the first time in *Arabidopsis* using *Ac/Ds* transposon or T-DNA-mediated mutagenesis. Having  
10 established the essentiality of the function of the encoded proteins in *Arabidopsis thaliana* and having identified the nucleotide sequences encoding these essential proteins, the inventors thereby provide an important and sought after tool for new herbicide development.

*Arabidopsis* insertional mutant lines segregating for seedling lethal mutations are identified as a first step in the identification of essential proteins. Starting with T2 seeds  
15 collected from single T1 plants containing T-DNA insertions in their genomes, those lines segregating homozygous seedling lethal seedlings are identified. *Ds* transposon insertion lines are produced as described in Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), incorporated herein by reference. Starting with F3 or F4 seeds collected from single F2 or F3 kanamycin-resistant plants containing *Ds* insertions in their genomes (see Figure 3 of  
20 Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), those lines segregating homozygous seedling lethal seedlings are identified. These lines are found by placing seeds onto minimal plant growth media, which contains the fungicides benomyl and maxim, and screening for inviable seedlings after 7 and 14 days in the light at room temperature. Inviably phenotypes include altered pigmentation or altered morphology. These phenotypes are observed either on  
25 plates directly or in soil following transplantation of seedlings.

Essential genes are also identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes or embryo. Gametophytic mutants are found by examining T1  
insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective  
30 mutants produce 25% defective seeds following self-pollination of T1 plants (see Errampalli *et al.* 1991, Plant Cell 3:149-157; Castle *et al.* 1993, Mol Gen Genet 241:504-514).

When a line is identified as segregating a seedling lethal or an embryo defective phenotype, it is determined if the resistance marker in the *Ds* transposon or T-DNA insertion co-segregates with the lethality (Errampalli *et al.* (1991) *The Plant Cell*, 3:149-157).

Cosegregation analysis is done by placing the seeds on media containing the selective agent and scoring the seedlings for resistance or sensitivity to the agent. Examples of selective agents used are kanamycin, hygromycin, or phosphinothricin. About 35 resistant seedlings are transplanted to soil and their progeny are examined for the segregation of the seedling lethal. In the case in which the *Ds* transposon or T-DNA insertion disrupts an essential gene, there is co-segregation of the resistance phenotype and the seedling lethal or embryo defective phenotype in every plant. Therefore, in such a case, all resistant plants segregate a seedling lethal or embryo defective phenotype in the next generation; this result indicates that each of the resistant plants is heterozygous for the mutation and hemizygous for the T-DNA insert causing the mutation.

For the *Arabidopsis* lines showing co-segregation of the transposon-encoded or T-DNA-encoded resistance marker and the lethal phenotype, PCR-based molecular approaches such as, TAIL-PCR (Liu *et al.* (1995) *Plant J.*, 8:457-463; Liu and Whittier (1995), *Genomics*, 25:674-681), TAIL2k, vectorette PCR (Riley *et al.* (1990) *Nucleic Acids Research*, 18: 2887-2890), or the GenomeWalker™ kit (CLONTECH Laboratories, Inc., Palo Alto, CA), may be used to directly amplify the plant DNA fragments flanking the transposon or T-DNA. Each of these techniques utilizes the known sequence of the transposon or T-DNA, and can be used to recover small (less than 5 kb) fragments directly adjacent to the insertion. PCR products are isolated and their DNA sequence is determined.

Alternatively, plasmid rescue may be used to isolate the plant DNA/T-DNA border fragments. Southern blot analysis may be performed as an initial step in the characterization of the molecular nature of each insertion. Southern blots are done with genomic DNA isolated from heterozygotes and using probes capable of hybridizing with the T-DNA vector DNA. Using the results of the Southern analysis, appropriate restriction enzymes are chosen to perform plasmid rescue in order to molecularly clone *Arabidopsis thaliana* genomic DNA flanking one or both sides of the T-DNA insertion. Plasmids obtained in this manner are analyzed by restriction enzyme digestion to sort the plasmids into classes based on their digestion pattern. For each class of plasmid clone, the DNA sequence is determined.

The resulting sequences, obtained by any of the above outlined approaches, are analyzed for the presence of non-*Ds* transposon and non-T-DNA vector sequences, as appropriate. When such sequences are found, they are used to search DNA and protein databases using the BLAST and BLAST2 programs (Altschul *et al.* (1990) *J Mol. Biol.* 215: 403-410; Altschul *et al.* (1997) *Nucleic Acid Res.* 25:3389-3402, both incorporated herein by reference). Additional genomic and cDNA sequences for each gene are identified by standard molecular biology procedures.

## II. Recombinant Production Of Essential Proteins And Uses Thereof

For recombinant production of a protein of the invention in a host organism, a nucleotide sequence encoding the protein is inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of the specific regulatory sequences such as promoter, signal sequence, 5' and 3' untranslated sequence, and enhancer appropriate for the chosen host is within the level of the skill of the routineer in the art. The resultant molecule, containing the individual elements linking in the proper reading frame, is inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli*, yeast, and insect cells (see, *e.g.*, Lucknow and Summers, *Bio/Technol.* 6:47 (1988)). Additional suitable expression vectors are baculovirus expression vectors, *e.g.*, those derived from the genome of *Autographica californica* nuclear polyhedrosis virus (AcMNPV). A preferred baculovirus/insect system is PVL1392(3) used to transfect *Spodoptera frugiperda* SF9 cells (ATCC) in the presence of linear *Autographica californica* baculovirus DNA (Phramingen, San Diego, CA). The resulting virus is used to infect HighFive *Tricoplusia ni* cells (Invitrogen, La Jolla, CA).

Recombinantly produced proteins are isolated and purified using a variety of standard techniques. The actual techniques used vary depending upon the host organism used, whether the protein is designed for secretion, and other such factors. Such techniques are well known to the skilled artisan (see, *e.g.* chapter 16 of Ausubel, F. *et al.*, "Current Protocols in Molecular Biology", pub. by John Wiley & Sons, Inc. (1994).

### III. Assays For Characterizing The Essential Proteins

The recombinantly produced proteins described herein are useful for a variety of purposes. For example, they can be used in *in vitro* assays to screen known herbicidal chemicals whose target has not been identified to determine if they inhibit protein activity.

5 Such *in vitro* assays may also be used as more general screens to identify chemicals that inhibit such protein activity and that are therefore novel herbicide candidates. Recombinantly produced proteins may also be used to elucidate the complex structure of these molecules and to further characterize their association with known inhibitors in order to rationally design new inhibitory herbicides. Alternatively, the recombinant protein can be used to isolate  
10 antibodies or peptides that modulate the activity and are useful in transgenic solutions.

### IV. *In vitro* Inhibitor Assay: Discovery of Small Molecule Ligands That Interact with Essential Proteins Of Unknown Biochemical Function

Once a protein has been identified as a potential herbicide target based on its  
15 essentiality for normal plant growth and viability, a next step is to develop an assay that allows screening large number of chemicals to determine which ones interact with the protein. Although it is straightforward to develop assays for proteins of known function, developing assays with proteins of unknown functions can be more difficult.

To address this issue, novel technologies are used that can detect interactions between  
20 a protein and a compound without knowing the biological function of the protein. A short description of three methods is presented, including fluorescence correlation spectroscopy, surface-enhanced laser desorption/ionization, and biacore technologies.

Fluorescence Correlation Spectroscopy (FCS) theory was developed in 1972 but it is only in recent years that the technology to perform FCS became available (Madge *et al.*  
25 (1972) Phys. Rev. Lett., 29: 705-708; Maiti *et al.* (1997) Proc. Natl. Acad. Sci. USA, 94: 11753-11757). FCS measures the average diffusion rate of a fluorescent molecule within a small sample volume. The sample size can be as low as  $10^3$  fluorescent molecules and the sample volume as low as the cytoplasm of a single bacterium. The diffusion rate is a function of the mass of the molecule and decreases as the mass increases. FCS can therefore be  
30 applied to protein-ligand interaction analysis by measuring the change in mass and therefore in diffusion rate of a molecule upon binding. In a typical experiment, the target to be analyzed is expressed as a recombinant protein with a sequence tag, such as a poly-histidine

sequence, inserted at the N or C-terminus. The expression takes place in *E. coli*, yeast or insect cells. The protein is purified by chromatography. For example, the poly-histidine tag can be used to bind the expressed protein to a metal chelate column such as Ni<sup>2+</sup> chelated on iminodiacetic acid agarose. The protein is then labeled with a fluorescent tag such as  
5 carboxytetramethylrhodamine or BODIPY® (Molecular Probes, Eugene, OR). The protein is then exposed in solution to the potential ligand, and its diffusion rate is determined by FCS using instrumentation available from Carl Zeiss, Inc. (Thornwood, NY). Ligand binding is determined by changes in the diffusion rate of the protein.

Surface-Enhanced Laser Desorption/Ionization (SELDI) was invented by Hutchens  
10 and Yip during the late 1980's (Hutchens and Yip (1993) *Rapid Commun. Mass Spectrom.* 7: 576-580). When coupled to a time-of-flight mass spectrometer (TOF), SELDI provides a mean to rapidly analyze molecules retained on a chip. It can be applied to ligand-protein interaction analysis by covalently binding the target protein on the chip and analyze by MS the small molecules that bind to this protein (Worrall *et al.* (1998) *Anal. Biochem.* 70: 750-  
15 756). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the SELDI chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via, for example, a delivery system capable to pipette the ligands in a sequential  
20 manner (autosampler). The chip is then submitted to washes of increasing stringency, for example a series of washes with buffer solutions containing an increasing ionic strength. After each wash, the bound material is analyzed by submitting the chip to SELDI-TOF. Ligands that specifically bind the target will be identified by the stringency of the wash needed to elute them.

25 Biacore relies on changes in the refractive index at the surface layer upon binding of a ligand to a protein immobilized on the layer. In this system, a collection of small ligands is injected sequentially in a 2-5 microlitre cell with the immobilized protein. Binding is detected by surface plasmon resonance (SPR) by recording laser light refracting from the surface. In general, the refractive index change for a given change of mass concentration at the surface  
30 layer, is practically the same for all proteins and peptides, allowing a single method to be applicable for any protein (Liedberg *et al.* (1983) *Sensors Actuators* 4: 299-304; Malmquist (1993) *Nature*, 361: 186-187). In a typical experiment, the target to be analyzed is expressed



as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the Biacore chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via the delivery system incorporated in the instruments  
5 sold by Biacore (Uppsala, Sweden) to pipette the ligands in a sequential manner (autosampler). The SPR signal on the chip is recorded and changes in the refractive index indicate an interaction between the immobilized target and the ligand. Analysis of the signal kinetics on rate and off rate allows the discrimination between non-specific and specific interaction.

10 Another assay for small molecule ligands that interact with a polypeptide is an inhibitor assay. For example, such an inhibitor assay useful for identifying inhibitors of the products of essential plant nucleic acid sequences, such as the essential *Arabidopsis* proteins described herein, comprises the steps of:

a) reacting an essential *Arabidopsis* protein described herein and a substrate thereof in  
15 the presence of a suspected inhibitor of the protein's function;

b) comparing the rate of enzymatic activity of the protein in the presence of the suspected inhibitor to the rate of enzymatic activity under the same conditions in the absence of the suspected inhibitor; and

c) determining whether the suspected inhibitor inhibits the essential *Arabidopsis*  
20 protein.

For example, the inhibitory effect on the activity of a hereindescribed essential *Arabidopsis* protein, may be determined by a reduction or complete inhibition of protein activity in the assay. Such a determination may be made by comparing, in the presence and absence of the candidate inhibitor, the amount of substrate used or intermediate or product  
25 made during the reaction.

## V. Production of peptides

Phage particles displaying diverse peptide libraries permits rapid library construction, affinity selection, amplification and selection of ligands directed against an essential protein  
30 (H.B. Lowman, *Annu. Rev. Biophys. Biomol. Struct.* 26, 401-424 (1997)). Structural analysis of these selectants can provide new information about ligand-target molecule interactions and

then in the process also provide a novel molecule that can enable the development of new herbicides based upon these peptides as leads.

#### VI. *In Vivo* Inhibitor Assay

5 In one embodiment, a suspected herbicide, for example identified by *in vitro* screening, is applied to plants at various concentrations. The suspected herbicide is preferably sprayed on the plants. After application of the suspected herbicide, its effect on the plants, for example death or suppression of growth is recorded.

10 In another embodiment, an *in vivo* screening assay for inhibitors of the activity of a hereindescribed essential protein uses transgenic plants, plant tissue, plant seeds or plant cells capable of overexpressing a nucleotide sequence disclosed herein that encodes an essential protein, wherein the essential protein is enzymatically active in the transgenic plants, plant tissue, plant seeds or plant cells. A chemical is then applied to the transgenic plants, plant tissue, plant seeds or plant cells and to the isogenic non-transgenic plants, plant tissue, plant seeds or plant cells, and the growth or viability of the transgenic and non-transformed plants, 15 plant tissue, plant seeds or plant cells are determined after application of the chemical and compared. Compounds capable of inhibiting the growth of the non-transgenic plants, but not affecting the growth of the transgenic plants are selected as specific inhibitors of the essential protein's activity.

20 The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

#### EXAMPLES

25 Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by J. Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual, 3d Ed.*, Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (2001); by T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. *et al.*, *Current Protocols in Molecular Biology*, New York, John Wiley and Sons Inc., (1988), Reiter, *et al.*, 30 *Methods in Arabidopsis Research*, World Scientific Press (1992), and Schultz *et al.*, *Plant Molecular Biology Manual*, Kluwer Academic Publishers (1998). These references describe

the standard techniques used for all steps in tagging and cloning genes from *Ac/Ds* transposon or T-DNA mutagenized populations of *Arabidopsis*: plant infection and transformation; screening for the identification of seedling mutants; and cosegregation analysis. *Ds* transposon insertion lines produced as described in Sundaresan *et al.* (1995) *Genes and Dev.*, 9:1797-1810) are used in these experiments. T-DNA lines are generated using vacuum infiltration or floral dip methods (Bechtold *et al.* (1993) *C. R. Acad. Sci. Paris*, 316:1194-1199; Clough and Bent (1998) *Plant J.*, 16:735-743; Desfeux *et al.* (2000) *Plant Physiol.*, 123:895-904).

10    Example 1:    Identification of *Arabidopsis* Mutants with Lethal Phenotypes

Essential genes are identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes, embryo, or resulting seedling. Gametophytic mutants are found by examining insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective lethal mutants usually produce 25% defective seeds following self-pollination of plants heterozygous for an insertion (see Errampalli *et al.* 1991, *Plant Cell* 3:149-157; Castle *et al.* 1993, *Mol Gen Genet* 241:504-514). Seedling lethal mutants usually segregate 25% seedlings that exhibit a lethal phenotype.

20    Example 2:    Cosegregation Analysis for Lines with Lethal Phenotypes

The linkage of the mutation to the *Ds* or T-DNA insertion is established after identifying a transformed line segregating for a lethal phenotype of interest. A line segregating with a single functional insert will segregate for resistance in the ratio of about 2:1 (resistant: sensitive) to the selectable marker. In the case of an embryo defective mutant, one-quarter of the progeny of a plant heterozygous for an insertion will fail to germinate due to embryo lethality, resulting in a reduction of the normal 3:1 ratio to 2:1. In the case of a seedling lethal mutant, the seedlings with a mutant phenotype are excluded in the calculation of this ratio. Each of the resistant progeny is therefore heterozygous for the mutation if the *Ds* or T-DNA insertion is causing the mutant phenotype. To establish cosegregation of the insertion and the mutant phenotype, about 30 resistant progeny are transplanted to soil and each plant is shown to segregate the 25% progeny with a lethal phenotype by the appropriate screening of embryo or seedlings. When all resistant plants segregate the lethal phenotype,

there is cosegregation of the insertion and the lethal mutation and the line is designated as "tagged."

Example 3: T-DNA Border Isolation by Plasmid Rescue

5           The plasmid rescue technique is used to molecularly clone *Arabidopsis* flanking DNA from one or both sides of the T-DNA insertion(s). *Arabidopsis* genomic DNA is isolated as described by Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992). Genomic DNA is digested with a restriction endonuclease and ligated overnight. After ligation, the DNA is transformed into competent *E. coli* strain XL-1 Blue, DH10B, DH5  
10   alpha, or the like, and colonies are selected on semi-solid medium containing ampicillin. Resistant colonies are picked into liquid medium with ampicillin and grown overnight. Plasmid DNA is isolated and digested with the rescue enzyme and analyzed on agarose gels containing ethidium bromide for visualization. Plasmids that represent different size classes are sequenced using primers that flank the plant DNA portion of the rescue element and the  
15   sequence is analyzed to determine what portion is plant DNA and what gene has been disrupted. The plasmid rescue is validated via PCR of template genomic DNA from a heterozygote for the insertion mutation. The experiment uses a primer anchored in the predicted flanking sequence and a primer in the T-DNA insertion. Finding a PCR product of the appropriate size, based on the sequence of the plasmid rescue clone confirms a valid  
20   rescue. Alternatively, Southern blot analysis with a probe that detects the relevant region of *Arabidopsis* DNA in genomic DNA from a heterozygote for the insertion mutation can be used to confirm the plasmid rescue results.

Example 4: Transposon or T-DNA Border Isolation by TAIL-PCR

25           *Arabidopsis* genomic DNA is isolated according to Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL-PCR technique (Liu *et al.* (1995) Plant J., 8:457-463; Liu and Whittier (1995), Genomics, 25:674-681). Three sets of  
30   12 TAIL-PCR reactions, referred to as the primary, secondary and tertiary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or

T-DNA-specific primer are used. The arbitrary degenerate primer is chosen from among seven primers, LWAD1, CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers are used in combination with two sets of three, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T-DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (tertiary primer) and left borders are recovered with JM33 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (tertiary primer) and left borders are recovered with JM33 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCVICEn4HPT (Hayashi *et al.* (1992), Science, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) Plant Physiol. 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (tertiary primer). When the degenerate and nested primer pairs are used in a series of low and high-stringency PCR amplifications, as described in the TAIL-PCR protocol (Liu and Whittier (1995), Genomics, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon or T-DNA insertion. The nucleic acid sequences of the PCR products from the tertiary TAIL-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-*Ds* transposon or non-T-DNA vector sequence.

To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone confirms a valid rescue.

Table 1: Arbitrary Degenerate Primers

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Degen.</u>	<u>Primer Sequence</u>
101	LWAD1	1026	ngt tgw gna twt sgw gnt
102	CA50	128	ngt cga swg ana wga a
5 103	CA51	128	tgw gna gsa nca sag a
104	CA52	128	agw gna gwa nca wag g
105	CA53	256	stt gnt ast nct ntg c
106	CA54	64	ntc gas twt sgw gtt
107	CA55	256	wgt gna gwa nca nag a

10

Table 2: Nested Primers For *Ds* Lines

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Primer Sequence</u>
108	5A	actagctctaccgtttccgtttccgtttac
109	5B	ttacctcgggttcgaaatcgatcgggataa
15 110	5C	aaaatcgggttatacgataacggtcgggtacggga
111	3A	gggtcttgcggatctgaatatatgtttcatgtgtg
112	3B	taccgaagaaaaataccggttcccgtccgatttcgac
113	3C	ggatcgtatcggttttcgattaccgtatttatcc

20 Table 3: Nested Primers For T-DNA Lines

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Primer Sequence</u>
114	CA66	att agg cac ccc agg ctt tac act tta tg
115	CA67	gta tgt tgt gtg gaa ttg tga gcg gat aac
116	CA68	taa caa ttt cac aca gga aac agc tat gac
25 117	JM33	tag cat ctg aat ttc ata acc aat ctc gat aca c
118	JM34	gct tcc tat tat atc ttc cca aat tac caa tac a
119	JM35	gcc ttt tca gaa atg gat aaa tag cct tgc ttc c
120	QRB1	caa act agg ata aat tat cgc gcg cgg tgt ca
121	QRB2	ggg gtc atc tat gtt act aga tgc gga att ga
30 122	QRB3	cgc cat ggc ata tgc tag cat gca taa ttc
123	SKI1	aat tgg taa tta ctc ttt ctt ttc ctc cat att ga
124	SKI2	ata ttg acc atc ata ctc att gct gat cca t
125	SKI3	tga tcc atg tag att tcc cgg aca tga a

Example 5: Transposon or T-DNA Border Isolation by TAIL2k PCR

*Arabidopsis* genomic DNA is isolated according to Reiter *et al.* in Methods in Arabidopsis Research, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL2k PCR technique. Two sets of 12 TAIL-PCR reactions, referred to as the primary and secondary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or T-DNA-specific primer are used. The arbitrary degenerate primer is selected from among six primers; CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers are used in combination with two sets of two, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T-DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (sequencing primer) and left borders are recovered with JM33 (sequencing primer), JM34 (secondary primer), and JM35 (primary primer). Primers CA66, CA67, and CA68 are also known as RB1, RB2, and RB3, respectively. Primers JM35, JM34, and JM33 are also known as LB1, LB2, and LB3, respectively. For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (sequencing primer) and left borders are recovered with JM33 (sequencing primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCVICEn4HPT (Hayashi *et al.* (1992), Science, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) Plant Physiol. 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (sequencing primer). When the degenerate and nested primer pairs are used in a series of low and high-stringency PCR amplifications, as described in the TAIL-PCR protocol (Liu and Whittier (1995), Genomics, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon

or T-DNA insertion. TAIL2k-PCR differs from the original TAIL-PCR protocol by the elimination of the tertiary PCR and modification of the secondary PCR. The cycling conditions used in the secondary reaction are modified to include 5 high annealing temperature cycles (64 degrees C) at the beginning, three additional so-called super cycles, and five additional low annealing temperature cycles (44 degrees C) at the end of the reaction. The melting and extension times are the same as all other TAIL-PCR reactions. Additionally, the reaction volume is increased to 40 microliters. The nucleic acid sequences of the PCR products from the secondary TAIL2k-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-*Ds* transposon or non-T-DNA vector sequence.

To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL2k-PCR sequencing result confirms a valid rescue.

#### Example 6: Identification of Both Borders of a T-DNA or *Ds* Insertion

If the results of border rescue provide information on only one of the two borders for an insertion in a given line, additional experiments are performed to identify the second border. These experiments are necessary to show that a single gene has been disrupted in a given line. In some cases, an insertion can affect more than a single gene due to a chromosomal deletion or rearrangement. In those cases, additional experiments are required to identify which of the affected genes is responsible for the lethal phenotype.

When both borders of an insertion are not recovered, primers are designed to isolate a PCR product that will provide information on the location of the missing border. Three primers are chosen in *Arabidopsis* genomic DNA on the opposite side of the insertion about one, two, and five kb away from the insertion point; the primers point towards the expected second border. Long PCR conditions (Advantage 2, Clontech) are then employed following the manufacturer's directions to amplify the relevant region from genomic DNA isolated from a heterozygote for the lethal mutation. PCR reactions are performed using appropriate pairs of genomic and T-DNA or *Ds* border primers. Finding a PCR product of the appropriate size,



based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point.

If the second border is not recovered with this method, an additional set of PCR reactions are preformed. In these experiments, the genomic primers are paired with a series of  
 5 internal T-DNA or *Ds* primers designed at about one kb intervals in both orientations across the entire T-DNA or *Ds* vector sequence. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point. Any borders recovered with this approach are classified as abnormal because they lack the  
 10 ends of the *Ds* transposon or the expected 24 bp T-DNA imperfect repeat characteristic of right and left borders.

#### Example 7: Identification of Insertion Points for Lines with Lethal Phenotypes

For each line with a lethal phenotype, the sequences of the borders of the insertion are  
 15 determined and the insertion points in the *Arabidopsis* genome are deduced. For *Ds* insertion lines, PCR products are obtained from the *Ds*3 and *Ds*5 borders. For T-DNA lines, PCR products or plasmid rescue clones are obtained from left (LB), right (RB), or abnormal (AB) borders. These sequences are used in BLASTn searches against nucleotide databases (Altschul *et al.* (1990) J Mol. Biol. 215:403-410; Altschul *et al.* (1997) Nucleic Acids Res.  
 20 25:3389-3402). The results are summarized in Table 4. *Ds* line names begin with ET or GT; T-DNA line names are numbers. The insertion point (Insert Pt.) and the direction of the flanking sequence (Dir.) either up (U) or down (D) in the genome section is noted. Often, small deletions or duplications of genomic DNA accompany the insertion of a T-DNA or *Ds* transposon.

25 The gene that has been inactivated in a given line with a lethal phenotype is determined from the insertion points for that line. Often, the precise location of an ORF for a given gene is not known, but predictions are available in genome sections deposited in GenBank. The precise boundaries of that ORF is determined as described in Example 7.

30 Table 4: Insertion Points For Lines With Lethal Phenotypes

Gene	Line #	Border	Genome Section	Acc. #	Insert Pt.	Dir.
942	942	LB	K24G6	AB012242	33667	D

978	978	LB	F23N20	AC016972	58221	D
	978	LB	F23N20	AC016972	58301	U
3218	3218	LB	T8K14	AC007202	10500	D
	3218	LB	T8K14	AC007202	10540	U
4563	4563	LB	ATCHRII092	AC006438	25542	D
8794	8794	LB	F2J6	AC009526	45854	D
	8794	LB	F2J6	AC009526	45879	U
9106	9106	LB	T2J13	AL132967	78013	U
	9106	AB	T2J13	AL132967	77943	D
10708	10708	RB	F1I21	AC005687	40005	D
	10708	LB	F1I21	AC005687	40042	U
	70241	LB	F1I21	AC005687	40210	D
	70241	RB	F1I21	AC005687	40215	U
10844	10844	LB	F13F21	AC007504	60873	U
	10844	LB	F13F21	AC007504	60839	D
10951	10951	LB	MKP11	AB005238	20298	D
	10951	LB	MKP11	AB005238	20318	U
12935	12935	LB	ATCHRII150	AC005168	36510	D
	12935	LB	ATCHRII150	AC005168	36545	U
13823	11361	LB	T27G7	AC006932	78096	U
	11361	AB	T27G7	AC006932	78065	D
	13823	LB	T27G7	AC006932	78096	U
	13823	RB	T27G7	AC006932	77722	D
14519	14519	LB	ATCHRIV72	AL161576	50259	U
	14519	AB	ATCHRIV72	AL161576	50228	D
14610.1	14610.1	LB	F4P13	AC009325	55319	U
	14610.1	RB	F4P13	AC009325	55442	D
14891	14891	LB	ATCHRIV89	AL161593	11412	U
	14891	RB	ATCHRIV89	AL161593	11313	D
14986	14986	LB	K10D20	AP000410	51816	D
	14986	RB	K10D20	AP000410	54505	U
15377	15377	RB	F28G11	AC074025	19572	D
	15377	LB	F28G11	AC074025	19587	U
16219	16219	LB	MRO11	AB005244	51998	U
	16219	LB	MRO11	AB005244	51995	D
16547	16547	LB	ATCHRIV65	AL161565	80692	D
	16547	RB	ATCHRIV65	AL161565	80791	U
20933	20933	LB	ATCHRII146	AC004747	47678	D
	20933	LB	ATCHRII146	AC004747	47683	U
21455	21455	LB	ATCHRIV54	AL161554	105596	U
	21455	RB	ATCHRIV54	AL161554	105542	D
21878	21878	LB	T19F11	AC009918	19609	D
23915	23915	LB	ATCHRII008	AC005936	49629	D
	23915	LB	ATCHRII008	AC005936	49657	U
30945	30945	LB	ATCHRII192	AC004238	2411	D
	30945	LB	ATCHRII192	AC004238	2410	U

31895	31895	LB	MTI20	AB013396	52020	D
	31895	LB	MTI20	AB013396	52089	U
34269	34269	LB	T4O12	AC007396	92811	U
	34269	RB	T4O12	AC007396	92808	D
34540	34540	LB	T1G11	AC002376	41572	D
	34540	LB	T1G11	AC002376	41608	U
	72902	LB	T1G11	AC002376	41494	U
	72902	LB	T1G11	AC002376	41465	D
34555	34555	LB	T1F15	AC004393	42152	D
	54334	RB	T1F15	AC004393	41803	U
	54334	LB	T1F15	AC004393	41671	D
35154	35154	RB	MWD9	AB007651	45718	D
	35154	LB	MWD9	AB007651	45732	U
35438	35438	LB	MAL21	AP000383	25170	D
	35438	LB	MAL21	AP000383	25738	U
37351	37351	LB	F25C20	AC007296	52890	U
	37351	RB	F25C20	AC007296	52196	D
37389	37389	LB	F3F19	AC007357	45488	U
	37389	RB	F3F19	AC007357	45471	D
38108	38108	LB	ATCHRII150	AC005168	83430	D
	38108	RB	ATCHRII150	AC005168	83446	U
43301	43301	RB	T22D16	AL357612	57549	D
	43301	LB	T22D16	AL357612	57599	U
46250	46250	LB	F17A9	AC016827	74222	D
	46250	RB	F17A9	AC016827	74274	U
47050A	47050	LB	T23E18	AC009978	49445	D
	47050	RB	T23E18	AC009978	49475	U
52949A	52949	LB	K16H17	AB016884	34713	D
	52949	LB	K16H17	AB016884	34718	U
53210A	53210	RB	ATCHRII017	AC007167	92796	D
	53210	LB	ATCHRII017	AC007167	92942	U
	69121	LB	ATCHRII017	AC007167	94478	D
	69121	LB	ATCHRII017	AC007167	94502	U
55483	55483	RB	ATCHRII164	AC005727	71269	U
	55483	LB	ATCHRII164	AC005727	71258	D
58351A	58351	RB	MYH9	AB016893	42547	D
	58351	LB	MYH9	AB016893	42772	U
60944	60944	LB	F1B16	AC023754	89492	U
	60944	LB	F1B16	AC023754	89428	D
62837	62837	LB	T21J18	AL132963	70906	U
	62837	LB	T21J18	AL132963	70873	D
65310	65310	LB	T20H2	AC022472	8158	U
	65310	RB	T20H2	AC022472	8096	D
68181	68181	RB	F12A12	AL133314	38270	U
	68181	LB	F12A12	AL133314	38275	D
70913	70913	LB	T24H18	AL353013	5347	D

	70913	LB	T24H18	AL353013	5358	U
71067	71067	LB	F2E2	AC069252	63031	U
	71067	LB	F2E2	AC069252	62932	D
71654	71654	RB	MYA6	AB023046	71956	U
	71654	LB	MYA6	AB023046	71907	D
ET3172	ET3172	DS5	ATCHRIV4	AL161492	134442	U
ET3546	ET3546	DS3	ATCHRII115	AC006081	20874	D
	ET3546	DS5	ATCHRII115	AC006081	20973	U

#### Example 8: Identification of cDNAs for Essential Genes

A cDNA for a gene identified as essential is identified using a variety of approaches. This information enables the ORF for a given gene to be identified and used for other experiments including expression of the corresponding protein in heterologous systems.

If there is a full-length cDNA deposited in GenBank or published elsewhere, that sequence may be checked independently using methods described below. Alternatively, the sequence may be considered to be correct.

In some cases, there are published EST sequences that can be assembled to cover the entire ORF from start codon to stop codon. This sequence may be checked independently using methods described below or it may be considered to be correct.

Often part of the cDNA is published and this information can be used to identify the entire ORF. If the 5' end containing the start codon is known, 3' RACE is performed to identify the remainder of the cDNA. If the 3' end containing the stop codon is known, 5' RACE is performed to identify the remainder of the cDNA. If both the 5' and the 3' ends are known, but the sequence between the two ends of the cDNA is not known, PCR is performed with primers hybridizing to each end of the cDNA. In all three of these cases, PCR is performed using template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

If no part of the cDNA is published, the cDNA is identified by starting from gene model predictions in the annotation for genomic clones or elsewhere. To identify the ORF, primers are designed to the 5' and 3' ends of the predicted ORF. PCR is performed using template DNA from a cDNA library prepared from seedling tissue or the pFL61 *Arabidopsis* cDNA library (Minet *et al.* (1992) Plant J. 2: 417-422). The resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced. Alternatively, 5' and 3' RACE are performed with primers predicted by gene models to be in exons. PCR is performed using

template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

- If the cDNA sequence is the same as the sequence predicted in the GenBank  
 5 annotation, the experiments confirm for the first time the actual ORF. If the cDNA sequence is not the same as the sequence predicted in the GenBank annotation, the experiments identify for the first time the actual ORF. In some cases, more than one cDNA sequence is found for a given gene and both sequences are included in this application.

#### 10 Example 9: Description of Essential Genes

- The putative function of the protein encoded by each essential gene is determined from analysis of the ORF in each cDNA. Information from the relevant *Arabidopsis* genomic section deposited in GenBank is used as a starting point to explore the function of a given gene. This analysis also includes BLAST searches (Altschul *et al.* (1990) J. Mol. Biol.  
 15 215:403-410; Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402) of sequence databases to identify similar proteins. Table 5 describes the putative functions for the essential genes discovered in this application.

Table 5: Putative Functions For Essential Genes

20

Gene	SEQ ID Nos:	Putative Function & Similar Genes	References
00942	1-2	similarity to disease resistance protein large gene family in <i>Arabidopsis</i> including disease resistance proteins RPP1-WsA,B&C; similar to tobacco TMV resistance protein N	Whitham, S. <i>et al.</i> (1994) Cell 78:1101-1115; Botella, M.A., <i>et al.</i> (1998) Plant Cell 10: 1847-1860
00978	3-4	unknown protein similar to <i>Arabidopsis</i> protein of unknown function (CAB87660) & ESTs from many plants	none
03218	5-6	AAA ATPase similar to <i>E. coli</i> FtsH cell division protein (P28691) that acts as an ATP-dependent metalloproteinase; homologs in many species	Schumann, W. (1999) FEMS Microbiol Rev 23:1-11; Langer, T. (2000) Trends Biochem Sci 25:247-251

04563	7-8	unknown protein large gene family in <i>Arabidopsis</i> of unknown function proteins	none
08794	9-10	putative histidine decarboxylase similar to Brassica, tomato (tom92), and rice putative histidine decarboxylases	Picton, S <i>et al.</i> (1993) <i>Plant Mol Biol</i> 23:627-631; Watanabe, T <i>et al.</i> (1990) <i>Trends Pharmacol Sci</i> 11:363- 367; Vaaler, G.L. & Snell, E.E. (1989) <i>Biochemistry</i> 28:7306-7313
09106	11-12	cytosolic 40S ribosomal protein S11-alpha	Browning, K.S. (1996) <i>Plant Mol Biol</i> 32:107-144; Gantt, J. S. & Thompson, M.D. (1990) <i>J. Biol Chem</i> 265:2763-2767
10708	13-14	cytoplasmic 60S ribosomal protein L3	Peltz, S.W. <i>et al.</i> (1999) <i>Mol Cell Biol</i> 19:384-391; Kim, Y. <i>et al.</i> (1990) <i>Gene</i> 93:177- 182; Wickner, R.B <i>et al.</i> (1982) <i>Proc Natl Acad Sci USA</i> 79:4706-4708
10844	15-16	40S ribosomal protein S17-like	Gantt, J.S. & Thompson, M.D. (1990) <i>J Biol Chem</i> 265:2763- 2767; Wiener, L. <i>et al.</i> (1988) <i>Nucleic Acids Res</i> 16:1233- 1250
10951	17-18	phytoene synthase	Welsch, R. <i>et al.</i> (2000) <i>Planta</i> 211:846-854; Shewmaker, C.K. <i>et al.</i> (1999) <i>Plant J.</i> 20:401-412; Von Lintig, J. <i>et al.</i> (1997) <i>Plant J.</i> 12:625-634
12935	19-20	putative choline kinase similar to soybean choline kinase (T08815) and mouse & human choline/ethanolamine kinases	Monks, D.E. <i>et al.</i> (1996) <i>Plant Physiol.</i> 110:1197-1205; Bligny, R. <i>et al.</i> (1989) <i>J Biol Chem.</i> 264:4888-4895; Wharfe, J. & Harwood, J.L. (1979) <i>Biochim Biophys Acta.</i> 575:102-111
13823	21-22	magnesium protoporphyrin IX chelatase subunit D	Papenbrock, J. <i>et al.</i> (1997) <i>Plant J.</i> 12:981-990; Papenbrock, J. <i>et al.</i> (2000) <i>Plant Physiol.</i> 122:1161-1169; Luo, M. <i>et al.</i> (1999) <i>Plant Mol Biol.</i> 41:721-731; Jensen, P.E. <i>et al.</i> (1996) <i>Mol. Gen. Genet.</i> 250:383-394

14519	23-24	putative protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
14610.1	25-26	putative cell division control protein; similar to cdc48, AAA ATPase proteins similar to <i>S. pombe</i> AAA ATPase (CAB16902); <i>Arabidopsis</i> cdc48 homolog (P54609); cdc48/valosin- containing protein homologs from soybean, <i>Capsicum annuum</i> , rice, <i>Dictyostelium</i> ; <i>Drosophila</i> smallminded	Frohlich, K.U. <i>et al.</i> (1991) J Cell Biol. 114:443-453; Feiler, H.S. <i>et al.</i> (1995) EMBO J. 14:5626-5637; Langer, T. (2000) Trends Biochem Sci 2000 25:247-251
14891	27-28	putative protein contains PFAM 02536 mTERF (mitochondrial transcription termination factor) domain; large gene family in <i>Arabidopsis</i> of unknown function proteins	Fernandez-Silva, P. <i>et al.</i> (1997) EMBO J 16:1066-1079
14986	29-30	ubiquitin isopeptidase T (aka ubiquitin-specific protease 14)	Wilkinson, K.D. <i>et al.</i> (1995) Biochemistry 34:14535- 14546; Falquet, L. <i>et al.</i> (1995) FEBS Lett 376:233- 237; Lindsey, D.F. <i>et al.</i> (1998) J Biol Chem 273:29178-29187
15377	31-32	putative formyl transferase similar to <i>B. napus</i> methionyl tRNA transformylase Fmt protein (AJ245479) & <i>B. rapa</i> S-locus protein 8 (AB022076)	Cui Y <i>et al.</i> (1999) Plant Cell. 11:2217-2231; Suzuki, G. <i>et al.</i> (1999) Genetics 153:391- 400; Cusack S. (1999) Curr Opin Struct Biol. 9:66-73
16219	33-34	polyadenylation cleavage/specificity factor 100 kDa subunit (AF283277)	Bilger, A. <i>et al.</i> (1994) Genes Dev. 8:1106-1116; Bienroth, S. <i>et al.</i> (1993) EMBO J. 12:585-594; Jenny, A. <i>et al.</i> (1994) Mol Cell Biol. 14:8183-8190
16547	35-36	similarity to UV-induced protein Uvi31, <i>S. pombe</i> , G1381578 unknown function, but similar to <i>Pectobacterium chrysanthemi</i> Sufe protein (AJ301654) involved in iron metabolism, <i>S. pombe</i> uvi31 protein of the BolA / YRBA family (Q12238), <i>Synechocystis</i> hypothetical 17.7 KDA protein SLR1419 (P74523)	Kim, S.H. <i>et al.</i> (1997) Environ Mol Mutagen 30:72- 81; Santos, J.M. <i>et al.</i> (1999) Mol Microbiol 32:789-798

20933	37-38	hypothetical protein contains WD40 repeats, similar to human CIAO 1 gene (O76071) & <i>S. cerevisiae</i> YDR267c (S70127)	Neer, E.J. <i>et al.</i> (1994) <i>Nature</i> 371:297-300; Johnstone, R.W. <i>et al.</i> (1998) <i>J Biol Chem</i> 273:10880-10887
21455	39-40	putative protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
21878	41-42	<i>Arabidopsis</i> digalactosyldiacylglycerol synthase (DGD1, AAD42378)	Dormann, P. <i>et al.</i> (1999) <i>Science</i> 284:2181-2184; Hartel, H. <i>et al.</i> (1997) <i>Plant</i> <i>Physiol</i> 115:1175-1184
23915	43-44	hypothetical protein contains PPR motifs, member of large gene family in <i>Arabidopsis</i>	Small, I.D. & Peeters, N. (2000) <i>Trends Biochem Sci</i> 25:46-47; Manthey, G.M. & McEwen, J.E. (1995) <i>EMBO J</i> 14:4031-4043; Barkan, A. <i>et</i> <i>al.</i> (1994) <i>EMBO J</i> 13:3170- 3181
30945	45-46	unknown protein similar to rice hypothetical protein (BAB56056)	none
31895	47-48	similar to unknown protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
34269	49-50	unknown protein	none
34540	51-52	probable lipote protein ligase B, similar to Mycobacterium LIPB gene (O32961) also similar to <i>S. pombe</i> putative pre-tRNA/pre-rRNA processing protein (T41635)	Reed, K.E. & Cronan, J.E. Jr. (1993) <i>J Bacteriol</i> 175:1325- 1336; Chen, X.J. (1997) <i>Mol.</i> <i>Gen. Genet.</i> 255:341-349
34555	53-54	similar to Synechocystis hypothetical 41.9KD protein (P52640) similar to several prokaryotic proteins of unknown function including <i>E. coli</i> YJEQ (P39286)	none
35154	55-56	similar to unknown protein similar to human hypothetical protein (BAA91556), <i>S. cerevisiae</i> probable membrane protein YOR262w (S67159), & <i>S. pombe</i> ATP(GTP)-binding protein Fet5 (AAC49837)	Shpakovskii, G.V. & Lebedenko, E.N. (1997) <i>Bioorg. Khim.</i> 23:234-237
35438	57-58	unknown protein weak similarity to <i>Pennisetum</i> <i>ciliare</i> unknown function protein (AAK15504)	none



37351	59-60	strong similarity to obtusifolios 14-alpha demethylase (CYP51; P93846) from <i>Sorghum bicolor</i> (also wheat & rice), member of the PFI00067 cytochrome P450 family	Kushiro, M. <i>et al.</i> (2001) <i>Biochem Biophys Res Commun.</i> 285:98-104; Bak <i>et al.</i> (1997) <i>Plant J.</i> 11:191-201; Grausem, B. (1995) <i>Plant J.</i> 7:761-770
37389	61-62	similar to human GLE1-like required for poly(A)+ RNA export (AAC25561)	Watkins, J.L. <i>et al.</i> (1998) <i>Proc. Natl. Acad. Sci. U.S.A.</i> 95:6779-6784; Murphy, R. & Went, S.R. (1996) <i>Nature</i> 383:357-360
38108	63-64	<i>Arabidopsis</i> 4-(cytidine 5'-phospho)-2-C-methyl-D-erythritol kinase (aka ispE & 4-diphosphocytidyl-2-C-methyl-Derythritol kinase) (AF288615) similar to <i>E. coli</i> ychB (aka ispE) gene (P24209)	Rohdich, F. <i>et al.</i> (2000) <i>Proc Natl Acad Sci U.S.A.</i> 97:8251-8256; Luetgen, H. <i>et al.</i> (2000) <i>Proc. Natl. Acad. Sci. U.S.A.</i> 97:1062-1067; Lange, B.M. & Croteau, R. (1999) <i>Proc Natl Acad Sci U.S.A.</i> 96:13714-13719
43301	65-66	similar to hypothetical bacterial proteins, including <i>Pseudomonas aeruginosa</i> protein PA0292 (F83608) & <i>Lactococcus lactis</i> (AAK05795)	none
46250	67-68	hypothetical protein weak similarity to hypothetical proteins from <i>Arabidopsis</i> (AAG51506) and mouse (BAB23375)	none
47050A	69-70	unknown protein weak similarity to Botrytis cDNA (AL115827)	none
52949A	71-72	6-phosphogluconolactonase-like protein similar to 6-phosphogluconolactonases such as human (O95336), <i>Brassica carinata</i> (AAK50346), & <i>Mycobacterium tuberculosis</i> (devB, CAB09261)	Collard, F. <i>et al.</i> (1999) <i>FEBS Lett.</i> 459:223-226; Bauer, H.P. <i>et al.</i> (1983) <i>Eur J Biochem.</i> 133:163-168
53210A	73-74	putative heat shock protein in hsp90 family similar to rye hsp82 (S65776), <i>Ipomoea nil</i> hsp83 (P51819), chicken hsp90 beta (Q04619) and others	Felsheim, R.F. & Das, A. (1992) <i>Plant Physiol.</i> 100:1764-1771; Coates, A.R. <i>et al.</i> (1999) <i>Biotechnol Genet Eng Rev</i> 16:393-405; Milioni, D. & Hatzopoulos, P. (1997) <i>Plant Mol Biol</i> 35:955-961

55483	75-76	putative para-aminobenzoate synthase and glutamine amidotransferase, a bifunctional enzyme similar to <i>Streptomyces pristinaespiralis</i> papA (AAC44866), <i>E. coli</i> pabB (P05041) & pabA (P00903), and <i>Bacillus stearothermophilus</i> anthranilate synthase component I trpE (AAD33791)	Goncharoff, P. & Nichols, B.P. (1984) <i>J Bacteriol.</i> 159:57-62.; Roux, B. & Walsh, C.T. (1992) <i>Biochemistry.</i> 31:6904-6910; Kaplan, J.B. & Nichols, B.P. (1983) <i>J Mol Biol</i> 168:451-468
58351A	77-78	26S proteasome p55 protein-like similar to human 26S proteasome regulatory complex chain p55 (BAA19749), <i>S. cerevisiae</i> 26S proteasome regulatory complex chain RPN5 (S67695), and others	Saito, A. <i>et al.</i> (1997) <i>Gene</i> 203:241-250; Glickman, M.H. <i>et al.</i> (1998) <i>Mol Cell Biol</i> 18:3149-3162
60944	79-80	similar to <i>Guillardia theta</i> chloroplast 50S ribosomal protein L31 (O46917)	Yamaguchi, K. & Subramanian, A.R. (2000) <i>J Biol Chem</i> , 275:28466-28482
62837	81-82	AtClpC: regulatory subunit of Clp protease with ATPase activity (BAA82062)	Adam, Z. (2000) <i>Biochimie</i> 82:647-654; Sokolenko, A. <i>et al.</i> (1998) <i>Planta</i> 207:286-295; Nakabayashi, K. <i>et al.</i> (1999) <i>Plant Cell Physiol.</i> 40:504-514; Maurizi, M.R. <i>et al.</i> (1990) <i>J Biol Chem.</i> 265:12536-12545
65310	83-84	26S proteasome regulatory subunit S3, contains a PCI PF01399 domain similar to 26S proteasome regulatory subunit S3 from <i>Nicotiana tabacum</i> (P93768), carrot (Q06364), human (O43242), <i>S. cerevisiae</i> RPN3 (P40016), and others	Voges, D. <i>et al.</i> (1999) <i>Ann Rev Biochem</i> 68:1015-1068; Fu, H. <i>et al.</i> (1999) <i>Mol Biol Rep</i> 26:137-146; Fu, H. <i>et al.</i> (1999) <i>Plant J</i> 18:529-539; Kominami, K. <i>et al.</i> (1997) <i>Mol Biol Cell</i> 8:171-187
68181	85-86	small zinc finger-like protein TIM9 similar to mitochondrial import inner membrane translocase subunit TIM9 from several plants and <i>S. cerevisiae</i> (O74700)	Koehler, C.M. <i>et al.</i> (1998) <i>EMBO J.</i> 17:6477-6486; Tokatlidis, K. <i>et al.</i> (2000) <i>Biochem Soc Trans</i> 28:495-499
70913	87-88	<i>Arabidopsis</i> CCAAT binding protein/transcription factor Hap2a (CAA74048)	Edwards, D. <i>et al.</i> (1998) <i>Plant Physiol</i> 117:1015-1022; Albani, D. & Robert, L.S. (1995) <i>Gene</i> 167:209-213

71067	89-90	hypothetical protein gene family in <i>Arabidopsis</i> of unknown function proteins	none
71654	91-92	poly(A) binding protein-like	Hilson, P. <i>et al.</i> (1993) <i>Plant Physiol</i> 103:525-533; Belostotsky, D.A. & Meagher, R.B. (1993) <i>Proc Natl Acad Sci U.S.A.</i> 90:6686-6690; Gallie, D.R. (1998) <i>Gene</i> 216:1-11
ET3172	93-94	hypothetical protein small gene family in <i>Arabidopsis</i> (T47999 & T02193) of unknown function	none
ET3546	95-96	cdc27/nuc2-like protein, may contain TPR-repeat similar to human cdc27 (P30260), <i>S. pombe</i> nuc2 (P10505), <i>S.</i> <i>cerevisiae</i> cdc23 (P16522), and others	Hirano, T. <i>et al.</i> (1988) <i>J. Cell Biol.</i> 106:1171-1183; Chen, P.L. <i>et al</i> (1995) <i>Cell Growth Differ.</i> 6:199-210

#### Example 10: Expression of Recombinant Essential Proteins in *E. coli*

The coding region of each of the essential proteins, corresponding to cDNA clones of  
5 odd-numbered SEQ ID NO:1-96, is subcloned into an appropriate expression vector, and  
transformed into *E. coli* using the manufacturer's conditions. Specific examples include  
plasmids such as pBluescript (Stratagene, La Jolla, CA), pFLAG (International  
Biotechnologies, Inc., New Haven, CT), and pTrcHis (Invitrogen, La Jolla, CA). *E. coli* is  
cultured, and expression of the essential protein is confirmed. Recombinant protein is isolated  
10 using standard techniques.

#### Example 11: *In Vitro* Binding Assays

Recombinant protein for each of the essential genes described in this application is  
obtained, for example, according to Example 10. The protein is immobilized on chips  
15 appropriate for ligand binding assays using techniques that are well known in the art. The  
protein immobilized on the chip is exposed to sample compound in solution according to  
methods well known in the art. While the sample compound is in contact with the immobilized  
protein, measurements capable of detecting protein-ligand interactions are conducted.  
Examples of such measurements are SELDI, biacore and FCS, described above. Compounds

found to bind the protein are readily discovered in this fashion and are subjected to further characterization.

5 The above-disclosed embodiments are illustrative. This disclosure of the invention will place one skilled in the art in possession of many variations of the invention. All such obvious and foreseeable variations are intended to be encompassed by the present invention.

CLAIMS:

1. A method of identifying a herbicidal compound, comprising:
  - a) combining a polypeptide comprising an amino acid sequence at least 90% identical  
5 to an amino acid sequence selected from the group consisting of the even  
numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind  
to said polypeptide, under conditions conducive to binding;
  - b) selecting a compound identified in (a) that binds to said polypeptide;
  - c) applying a compound selected in (b) to a plant to test for herbicidal activity; and
  - 10 d) selecting a compound identified in (c) that has herbicidal activity.
2. The method according to claim 1, wherein said polypeptide comprises an amino acid  
sequence at least 95% identical to an amino acid sequence selected from the group consisting  
of the even numbered SEQ ID NOs:2-96.  
15
3. The method according to claim 2, wherein said polypeptide comprises an amino acid  
sequence at least 99% identical to an amino acid sequence selected from the group consisting  
of the even numbered SEQ ID NOs:2-96.
- 20 4. The method according to claim 3, wherein said polypeptide comprises an amino acid  
sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
5. A method of identifying a herbicidal compound, comprising:
  - c) combining a polypeptide comprising an amino acid sequence at least 90% identical  
25 to an amino acid sequence selected from the group consisting of the even  
numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit  
the activity of said polypeptide, under conditions conducive to inhibition;
  - d) selecting a compound identified in (a) that inhibits the activity of said polypeptide;
  - c) applying a compound selected in (b) to a plant to test for herbicidal activity; and
  - 30 d) selecting a compound identified in (c) that has herbicidal activity.

6. The method according to claim 5, wherein said polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
- 5 7. The method according to claim 6, wherein said polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
8. The method according to claim 7, wherein said polypeptide comprises an amino acid  
10 sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
9. A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 1.
- 15 10. A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 5.

# SEQUENCE LISTING

<110> Syngenta Participations AG

<120> NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

<130> 60035A

<150> US 60/305,806

<151> 2001-07-16

<150> US 60/358,416

<151> 2002-02-20

<160> 125

&lt;170&gt; PatentIn version 3.1

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<211> 2010

<212> DNA

<213> Arabidopsis thaliana

**<220>**

<221> CDS

<222> (1) .. (2010)

<223> 942

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 245 250 255  
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 260 265 270

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Asn Glu Ser Phe Asp Pro Ile Arg Lys Leu Ala Arg Val Ile Ser Ser  
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His Pro Phe Leu Gly Phe Glu Asp Leu Ser Cys Arg Ala Val Lys Leu  
 355 360 365

Ala Gly Gly Phe Pro Leu Ser Leu Lys Arg Leu Gly Ser Arg Phe Ser  
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Gly Arg Lys Lys Asp Glu Trp Glu Val Ile Leu Phe Gly Tyr Glu Arg  
 385 390 395 400

Ser Thr Val Asn Gly Val Ile Asn Pro Glu Lys Asn Ser Leu Asp Gly  
 405 410 415

Leu Tyr Glu Tyr Ser Ser Ile Met Glu Thr Phe Ser Ser Gln Pro Ile  
 420 425 430

Ser Ser Thr Thr Arg Ser Phe Glu Asp Leu Val Gly Met Asn His Arg  
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Met Gln Ala Leu Ser Ala Leu Leu Glu Leu Glu Ser Asp Lys Glu Val  
 450 455 460

Arg Val Val Gly Ile Trp Gly Thr Gly Gly Ile Gly Lys Thr Thr Leu  
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Ser Arg Tyr Ala Tyr Glu Arg Ile Ser Gln Gln Phe His Thr His Ala  
 485 490 495

Phe Leu Glu Asn Ala Gln Glu Ser Ser Ser Ser Cys Leu Glu Glu Arg  
 500 505 510

Phe Leu Ser Lys Ala Ile Gln Arg Glu Ala Leu Ala Val Arg Asn Ser  
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Lys Asp Cys Pro Glu Ile Met Lys Ser Leu Ile Gln His Arg Lys Val  
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Leu Leu Ile Val Asp Asp Val Asp Asn Val Lys Thr Leu Glu Glu Val  
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Phe Lys Ile Thr Ser Trp Leu Val Pro Gly Ser Arg Val Ile Val Thr  
 565 570 575

Ala Arg Asp Glu Ser Phe Leu Leu Ala Ser Gly Val Lys Tyr Ile Phe  
 580 585 590

Glu Val Lys Gly Leu Arg Phe Asp Gln Ala Leu Gln Leu Phe Tyr Gln  
 595 600 605

Phe Ala Phe Lys Gln Lys Ser Pro Pro Val Arg Phe Arg Gln Leu Ser  
 610 615 620

Val Arg Ala Ile Lys Leu Val Gly Phe Leu Pro Leu Ala Leu Lys Val  
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Thr Gly Ser Met Leu Tyr Arg Lys Lys Glu Ser Tyr Trp Glu Thr Ile  
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ata ata ctt atg atc gtc act ccc aca atc cct caa tct cag gct tac	96
Ile Ile Leu Met Ile Val Thr Pro Thr Ile Pro Gln Ser Gln Ala Tyr	
20 25 30	
cac aat ttc gcc gat caa cgc tcc ttc ttc ggg att cca aat ttt tta	144
His Asn Phe Ala Asp Gln Arg Ser Phe Phe Gly Ile Pro Asn Phe Leu	
35 40 45	
aac gtc atc tcc aac ttc cct ttc ctc atc atc ggc ttt atc ggt ctt	192
Asn Val Ile Ser Asn Phe Pro Phe Leu Ile Ile Gly Phe Ile Gly Leu	
50 55 60	
atc ctc tgc ttt tac cca gaa gat tac ttt agc ttt agt ttg cga ggt	240
Ile Leu Cys Phe Tyr Pro Glu Asp Tyr Phe Ser Phe Ser Leu Arg Gly	
65 70 75 80	
gag aaa ata gga tgg act tgc ttt tac atc ggt gta gct gct gtt gct	288
Glu Lys Ile Gly Trp Thr Cys Phe Tyr Ile Gly Val Ala Ala Val Ala	
85 90 95	
ttt gga tct tct tac tat cat ctt cac cca aac gat gct act ctc ctc	336
Phe Gly Ser Ser Tyr Tyr His Leu His Pro Asn Asp Ala Thr Leu Leu	
100 105 110	
tgg gat cgt ctt ccc atg act att gct ttc aca tca atc atg gct ata	384
Trp Asp Arg Leu Pro Met Thr Ile Ala Phe Thr Ser Ile Met Ala Ile	
115 120 125	
ttt gta atc gag agg att gat gag cat aag ggt act tac tcc att gct	432
Phe Val Ile Glu Arg Ile Asp Glu His Lys Gly Thr Tyr Ser Ile Ala	
130 135 140	
cct tta ctt ctt gct ggt ctt gtt agc att ttg tat tgg agg ttt ttc	480
Pro Leu Leu Leu Ala Gly Leu Val Ser Ile Leu Tyr Trp Arg Phe Phe	
145 150 155 160	
gat gac ctt agg cca tat gct ttg gtt cag ttt gtt cct tgc att gtg	528
Asp Asp Leu Arg Pro Tyr Ala Leu Val Gln Phe Val Pro Cys Ile Val	
165 170 175	
att ccg ttg atg gct att tta ttg cct cca atg tat aca cat tcc act	576
Ile Pro Leu Met Ala Ile Leu Leu Pro Pro Met Tyr Thr His Ser Thr	
180 185 190	
tat tgg cta tgg gct gca ggg ttc tat ctc tta gcc aag gtg gaa gaa	624
Tyr Trp Leu Trp Ala Ala Gly Phe Tyr Leu Leu Ala Lys Val Glu Glu	
195 200 205	
gct gcg gat aag cct ata tat agc tgg act cat cat att att agt ggg	672
Ala Ala Asp Lys Pro Ile Tyr Ser Trp Thr His His Ile Ile Ser Gly	
210 215 220	
cat tct ctg aag cat ttg tgt gcc gct atg gtc cct gtc ttc ctt acc	720
His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr	
225 230 235 240	

ctc atg ctt gcg aaa aga acc gtt caa act gag agg att agc ttg tat 768  
 Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr  
                   245                                  250                                  255

aag aca tgg aag aaa gga tcc gag gaa gaa cgg ttc gag cat agc tac 816  
 Lys Thr Trp Lys Lys Gly Ser Glu Glu Glu Arg Phe Glu His Ser Tyr  
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                   20                                  25                                  30

His Asn Phe Ala Asp Gln Arg Ser Phe Phe Gly Ile Pro Asn Phe Leu  
                   35                                  40                                  45

Asn Val Ile Ser Asn Phe Pro Phe Leu Ile Ile Gly Phe Ile Gly Leu  
                   50                                  55                                  60

Ile Leu Cys Phe Tyr Pro Glu Asp Tyr Phe Ser Phe Ser Leu Arg Gly  
 65                                  70                                  75                                  80

Glu Lys Ile Gly Trp Thr Cys Phe Tyr Ile Gly Val Ala Ala Val Ala  
                   85                                  90                                  95

Phe Gly Ser Ser Tyr Tyr His Leu His Pro Asn Asp Ala Thr Leu Leu  
                   100                                  105                                  110

Trp Asp Arg Leu Pro Met Thr Ile Ala Phe Thr Ser Ile Met Ala Ile  
                   115                                  120                                  125

Phe Val Ile Glu Arg Ile Asp Glu His Lys Gly Thr Tyr Ser Ile Ala  
                   130                                  135                                  140

Pro Leu Leu Leu Ala Gly Leu Val Ser Ile Leu Tyr Trp Arg Phe Phe  
145 150 155 160

Asp Asp Leu Arg Pro Tyr Ala Leu Val Gln Phe Val Pro Cys Ile Val  
165 170 175

Ile Pro Leu Met Ala Ile Leu Leu Pro Pro Met Tyr Thr His Ser Thr  
180 185 190

Tyr Trp Leu Trp Ala Ala Gly Phe Tyr Leu Leu Ala Lys Val Glu Glu  
195 200 205

Ala Ala Asp Lys Pro Ile Tyr Ser Trp Thr His His Ile Ile Ser Gly  
210 215 220

His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr  
225 230 235 240

Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr  
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Thr	Gln	Leu	Leu	Lys	Arg	Ser	Lys	Ser	Phe	Gly	Leu	Val	Arg	Phe	Pro	
			20					25					30			
gcc	aag	tat	gga	ctg	gga	gct	acc	cgg	aaa	aaa	cag	ctc	ttt	cga	gtc	144
Ala	Lys	Tyr	Gly	Leu	Gly	Ala	Thr	Arg	Lys	Lys	Gln	Leu	Phe	Arg	Val	
		35				40						45				
tat	gcg	tct	gaa	agt	agt	agt	ggg	tct	tca	tct	aat	agc	gat	gga	ggc	192
Tyr	Ala	Ser	Glu	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Asn	Ser	Asp	Gly	Gly	
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Phe	Ser	Trp	Val	Arg	Leu	Ala	Gln	Ser	Ile	Arg	Leu	Gly	Ala	Glu	Arg	
65					70					75					80	
att	ggg	gag	aag	att	gga	gaa	tct	gtg	aag	aca	gaa	att	ggg	ttt	gac	288
Ile	Gly	Glu	Lys	Ile	Gly	Glu	Ser	Val	Lys	Thr	Glu	Ile	Gly	Phe	Asp	
				85					90					95		
tcg	gaa	gaa	gca	agt	ggg	aga	gtg	aat	gag	tat	gtg	gct	cga	gtt	aag	336
Ser	Glu	Glu	Ala	Ser	Gly	Arg	Val	Asn	Glu	Tyr	Val	Ala	Arg	Val	Lys	
			100					105					110			
gat	agt	gtg	cac	aag	ggc	cat	cac	gag	ctg	act	cgc	ttt	aag	aat	gag	384
Asp	Ser	Val	His	Lys	Gly	His	His	Glu	Leu	Thr	Arg	Phe	Lys	Asn	Glu	
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aca	gtg	cct	tcg	ttt	att	gat	tgg	aac	aag	tgg	gag	cat	tgg	aag	gac	432
Thr	Val	Pro	Ser	Phe	Ile	Asp	Trp	Asn	Lys	Trp	Glu	His	Trp	Lys	Asp	
	130					135					140					
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Ile	Arg	Asn	Trp	Asp	Gly	Lys	Arg	Val	Ala	Ala	Leu	Phe	Ile	Tyr	Ala	
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Phe	Ala	Leu	Leu	Leu	Ser	Cys	Gln	Arg	Val	Tyr	Val	Ala	Ile	Gln	Ala	
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cct	cgg	gta	gaa	cga	gag	aga	aga	gag	tta	aca	gag	tct	ttt	atg	gag	576
Pro	Arg	Val	Glu	Arg	Glu	Arg	Arg	Glu	Leu	Thr	Glu	Ser	Phe	Met	Glu	
			180					185					190			
gct	ttg	atc	ccc	gag	cca	tct	cct	gga	aat	ata	gaa	aag	ttc	aag	aga	624
Ala	Leu	Ile	Pro	Glu	Pro	Ser	Pro	Gly	Asn	Ile	Glu	Lys	Phe	Lys	Arg	
		195					200					205				
aat	atg	tgg	agg	aaa	gca	aca	cct	aaa	ggc	ttg	aaa	tta	aaa	agg	ttc	672
Asn	Met	Trp	Arg	Lys	Ala	Thr	Pro	Lys	Gly	Leu	Lys	Leu	Lys	Arg	Phe	
	210					215					220					
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Ile	Glu	Ala	Pro	Asp	Gly	Thr	Leu	Val	His	Asp	Ser	Ser	Tyr	Val	Gly	
225						230				235					240	
gaa	aat	gcg	tgg	gat	gac	gat	cta	gag	acc	aca	gag	gga	tct	ctc	aag	768

Glu	Asn	Ala	Trp	Asp	Asp	Asp	Leu	Glu	Thr	Thr	Glu	Gly	Ser	Leu	Lys	
				245					250					255		
aaa	ata	att	ggt	aga	aat	gct	agg	att	cag	aca	gag	gca	aag	aag	aaa	816
Lys	Ile	Ile	Gly	Arg	Asn	Ala	Arg	Ile	Gln	Thr	Glu	Ala	Lys	Lys	Lys	
			260					265					270			
cta	agc	caa	gat	ctg	ggt	gtc	tct	ggt	gaa	att	gga	gac	agt	gta	ggt	864
Leu	Ser	Gln	Asp	Leu	Gly	Val	Ser	Gly	Glu	Ile	Gly	Asp	Ser	Val	Gly	
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Asn	Trp	Arg	Glu	Arg	Leu	Ala	Thr	Trp	Lys	Glu	Met	Leu	Glu	Arg	Glu	
290						295				300						
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Lys	Leu	Ser	Glu	Gln	Leu	Asn	Ser	Ser	Ala	Ala	Lys	Tyr	Val	Val	Glu	
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Phe	Asp	Met	Lys	Glu	Val	Glu	Lys	Ser	Leu	Arg	Glu	Asp	Val	Ile	Gly	
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agg	aca	tct	gaa	act	gag	gga	act	aga	gct	ctc	tgg	ata	tca	aag	aga	1056
Arg	Thr	Ser	Glu	Thr	Glu	Gly	Thr	Arg	Ala	Leu	Trp	Ile	Ser	Lys	Arg	
			340					345					350			
tgg	tgg	cga	tat	cgc	cct	aag	ctt	ccc	tat	acc	tac	ttc	ctt	cag	aag	1104
Trp	Trp	Arg	Tyr	Arg	Pro	Lys	Leu	Pro	Tyr	Thr	Tyr	Phe	Leu	Gln	Lys	
		355					360					365				
ctt	gat	tct	tct	gag	gtt	gca	gct	gtt	gtt	ttc	acg	gaa	gac	cta	aag	1152
Leu	Asp	Ser	Ser	Glu	Val	Ala	Ala	Val	Val	Phe	Thr	Glu	Asp	Leu	Lys	
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aga	ttg	tat	gtg	acc	atg	aaa	gaa	ggt	ttc	cct	cta	gaa	tat	att	gtt	1200
Arg	Leu	Tyr	Val	Thr	Met	Lys	Glu	Gly	Phe	Pro	Leu	Glu	Tyr	Ile	Val	
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Asp	Ile	Pro	Leu	Asp	Pro	Tyr	Leu	Phe	Glu	Thr	Ile	Cys	Asn	Ala	Gly	
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gtt	gag	gtg	gat	ctt	ctt	cag	aag	agg	cag	atc	cac	tac	ttc	atg	aaa	1296
Val	Glu	Val	Asp	Leu	Leu	Gln	Lys	Arg	Gln	Ile	His	Tyr	Phe	Met	Lys	
			420					425					430			
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Val	Phe	Ile	Ala	Leu	Leu	Pro	Gly	Ile	Leu	Ile	Leu	Trp	Phe	Ile	Arg	
		435					440					445				
gaa	tct	gcc	atg	ctt	ctc	ctt	atc	aca	tcc	aag	cgc	ttt	ctc	tac	aag	1392
Glu	Ser	Ala	Met	Leu	Leu	Leu	Ile	Thr	Ser	Lys	Arg	Phe	Leu	Tyr	Lys	
	450					455				460						
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Lys	Tyr	Asn	Gln	Leu	Phe	Asp	Met	Ala	Tyr	Ala	Glu	Asn	Phe	Ile	Leu	
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Pro	Val	Gly	Asp	Val	Ser	Glu	Thr	Lys	Ser	Met	Tyr	Lys	Glu	Val	Val	
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Leu	Gly	Gly	Asp	Val	Trp	Asp	Leu	Leu	Asp	Glu	Leu	Met	Ile	Tyr	Met	
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Gly	Asn	Pro	Met	Gln	Tyr	Tyr	Glu	Lys	Asp	Val	Ala	Phe	Val	Arg	Gly	
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gtg	ctt	ctt	tct	gga	cct	cct	gga	act	gga	aaa	aca	ctt	ttt	gcg	cga	1632
Val	Leu	Leu	Ser	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Phe	Ala	Arg	
	530					535					540					
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Thr	Leu	Ala	Lys	Glu	Ser	Gly	Leu	Pro	Phe	Val	Phe	Ala	Ser	Gly	Ala	
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Glu	Phe	Thr	Asp	Ser	Glu	Lys	Ser	Gly	Ala	Ala	Lys	Ile	Asn	Glu	Met	
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Phe	Ser	Ile	Ala	Arg	Arg	Asn	Ala	Pro	Ala	Phe	Val	Phe	Val	Asp	Glu	
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Ile	Asp	Ala	Ile	Ala	Gly	Arg	His	Ala	Arg	Lys	Asp	Pro	Arg	Arg	Arg	
		595				600						605				
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Ala	Thr	Phe	Glu	Ala	Leu	Ile	Ala	Gln	Leu	Asp	Gly	Glu	Lys	Glu	Lys	
	610					615					620					
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gct	acc	aat	aga	cct	gat	gaa	ctc	gac	ctt	gag	ttt	gtc	cgt	tct	ggc	1968
Ala	Thr	Asn	Arg	Pro	Asp	Glu	Leu	Asp	Leu	Glu	Phe	Val	Arg	Ser	Gly	
				645					650					655		
cgt	att	gac	cgt	cgg	ctg	tat	att	ggg	ttg	cct	gat	gca	aag	caa	agg	2016
Arg	Ile	Asp	Arg	Arg	Leu	Tyr	Ile	Gly	Leu	Pro	Asp	Ala	Lys	Gln	Arg	
			660					665					670			
gtg	caa	ata	ttt	gga	gtt	cac	agt	gct	ggg	aag	aac	ctt	gca	gaa	gat	2064
Val	Gln	Ile	Phe	Gly	Val	His	Ser	Ala	Gly	Lys	Asn	Leu	Ala	Glu	Asp	
		675					680					685				
ata	gac	ttt	ggg	aag	ctt	gtt	ttt	cga	acg	gtt	ggc	ttt	tcc	ggg	gca	2112
Ile	Asp	Phe	Gly	Lys	Leu	Val	Phe	Arg	Thr	Val	Gly	Phe	Ser	Gly	Ala	
	690					695					700					
gat	atc	cgg	aat	ctt	gtt	aac	gaa	gcg	gct	ata	atg	tcg	gta	agg	aag	2160
Asp	Ile	Arg	Asn	Leu	Val	Asn	Glu	Ala	Ala	Ile	Met	Ser	Val	Arg	Lys	
705					710					715					720	
gga	cgt	tct	tac	ata	tat	caa	caa	gac	att	gtt	gat	gtg	tta	gat	aaa	2208

Gly	Arg	Ser	Tyr	Ile	Tyr	Gln	Gln	Asp	Ile	Val	Asp	Val	Leu	Asp	Lys	
				725					730						735	
caa	ttg	ctc	gag	ggg	atg	ggg	gta	ctt	ctt	aca	gag	gaa	gag	caa	cag	2256
Gln	Leu	Leu	Glu	Gly	Met	Gly	Val	Leu	Leu	Thr	Glu	Glu	Glu	Gln	Gln	
			740					745					750			
aaa	tgt	gaa	caa	agt	gta	tct	tac	gaa	aag	aag	aga	ctt	ctg	gct	gtt	2304
Lys	Cys	Glu	Gln	Ser	Val	Ser	Tyr	Glu	Lys	Lys	Arg	Leu	Leu	Ala	Val	
		755					760					765				
cat	gag	gct	ggg	cat	ata	gtg	ttg	gct	cat	ttg	ttt	cct	cga	ttt	gac	2352
His	Glu	Ala	Gly	His	Ile	Val	Leu	Ala	His	Leu	Phe	Pro	Arg	Phe	Asp	
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Trp	His	Ala	Phe	Ser	Gln	Leu	Leu	Pro	Gly	Gly	Lys	Glu	Thr	Ala	Val	
785					790				795						800	
tcg	gtt	ttc	tat	cca	cgt	gaa	gac	atg	gta	gac	caa	ggg	tat	acc	acg	2448
Ser	Val	Phe	Tyr	Pro	Arg	Glu	Asp	Met	Val	Asp	Gln	Gly	Tyr	Thr	Thr	
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ttt	ggg	tat	atg	aaa	atg	caa	atg	gtg	gta	gct	cat	ggg	gga	cgc	tgt	2496
Phe	Gly	Tyr	Met	Lys	Met	Gln	Met	Val	Val	Ala	His	Gly	Gly	Arg	Cys	
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gct	gaa	cgt	gtg	gtt	ttt	ggc	gat	aat	gtc	act	gat	gga	gga	aaa	gat	2544
Ala	Glu	Arg	Val	Val	Phe	Gly	Asp	Asn	Val	Thr	Asp	Gly	Gly	Lys	Asp	
		835					840					845				
gac	ctg	gag	aag	ata	aca	aaa	att	gcc	agg	gag	atg	gtg	att	agc	cct	2592
Asp	Leu	Glu	Lys	Ile	Thr	Lys	Ile	Ala	Arg	Glu	Met	Val	Ile	Ser	Pro	
	850					855					860					
caa	agt	gcg	aga	tta	ggg	ctc	act	caa	ctt	gta	aaa	aag	att	gga	atg	2640
Gln	Ser	Ala	Arg	Leu	Gly	Leu	Thr	Gln	Leu	Val	Lys	Lys	Ile	Gly	Met	
865					870					875					880	
gtg	gat	tta	cca	gat	aac	cca	gac	ggc	gag	ctg	ata	aaa	tac	cgg	tgg	2688
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Leu	Phe	Thr	Arg	Glu	Leu	Thr	Arg	Tyr	Ile	Glu	Glu	Thr	Glu	Glu	Leu	
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gcg	atg	aat	gct	ctg	aga	gca	aac	agg	cac	att	ctg	gac	tta	atc	acc	2832
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Arg	Glu	Leu	Leu	Glu	Lys	Ser	Arg	Ile	Thr	Gly	Leu	Glu	Val	Glu	Glu	
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Phe Ala Leu Leu Leu Ser Cys Gln Arg Val Tyr Val Ala Ile Gln Ala  
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Pro Arg Val Glu Arg Glu Arg Arg Glu Leu Thr Glu Ser Phe Met Glu  
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Ala Leu Ile Pro Glu Pro Ser Pro Gly Asn Ile Glu Lys Phe Lys Arg  
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Asn Met Trp Arg Lys Ala Thr Pro Lys Gly Leu Lys Leu Lys Arg Phe  
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Ile Glu Ala Pro Asp Gly Thr Leu Val His Asp Ser Ser Tyr Val Gly  
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Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys  
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Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly  
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Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu  
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Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly  
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Val Phe Ile Ala Leu Leu Pro Gly Ile Leu Ile Leu Trp Phe Ile Arg  
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Gly Arg Ser Tyr Ile Tyr Gln Gln Asp Ile Val Asp Val Leu Asp Lys  
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Gln Leu Leu Glu Gly Met Gly Val Leu Leu Thr Glu Glu Glu Gln Gln  
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Trp His Ala Phe Ser Gln Leu Leu Pro Gly Gly Lys Glu Thr Ala Val  
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Gln Ser Ala Arg Leu Gly Leu Thr Gln Leu Val Lys Lys Ile Gly Met  
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Val Asp Leu Pro Asp Asn Pro Asp Gly Glu Leu Ile Lys Tyr Arg Trp  
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Asp His Pro His Val Met Pro Ala Glu Met Ser Val Glu Val Ser Glu  
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Ala Met Asn Ala Leu Arg Ala Asn Arg His Ile Leu Asp Leu Ile Thr  
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Arg Glu Leu Leu Glu Lys Ser Arg Ile Thr Gly Leu Glu Val Glu Glu  
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Thr Arg Thr Pro Pro Leu Phe Thr Ala Asn Ser Thr Ala Gln Arg Ser  
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Gly Thr Phe Val Glu His Leu Thr Gly Ile Thr Glu Ser Glu Glu Gly  
 115 120 125

Ile Ser Glu Ala Asn Gly Phe Gly Asp Val Glu Ser Ala Arg Asn Asp  
 130 135 140

Ile Arg Asn Val Ala Thr Arg Arg Ile Glu Thr Glu Phe Glu Val Arg  
 145 150 155 160

Glu Leu Glu Glu Leu Pro Glu Glu Trp Arg Arg Ser Lys Leu Ala Trp  
 165 170 175

Leu Cys Lys Glu Val Pro Thr His Lys Ala Val Thr Leu Val Arg Leu  
 180 185 190

Leu Asn Ala Gln Lys Lys Trp Val Arg Gln Glu Asp Ala Thr Tyr Ile  
 195 200 205

Ser Val His Cys Met Arg Ile Arg Glu Asn Glu Thr Gly Phe Arg Val  
 210 215 220

Tyr Arg Trp Met Thr Gln Gln Asn Trp Tyr Arg Phe Asp Phe Gly Leu  
 225 230 235 240

Thr Thr Lys Leu Ala Glu Tyr Leu Gly Lys Glu Arg Lys Phe Thr Lys  
 245 250 255

Cys Arg Glu Val Phe Asp Asp Val Leu Asn Gln Gly Arg Val Pro Ser  
 260 265 270

Glu Ser Thr Phe His Ile Leu Val Val Ala Tyr Leu Ser Ser Leu Ser  
 275 280 285

Val Glu Gly Cys Leu Glu Glu Ala Cys Ser Val Tyr Asn Arg Met Ile  
 290 295 300

Gln Leu Gly Gly Tyr Lys Pro Arg Leu Ser Leu His Asn Ser Leu Phe  
 305 310 315 320

Arg Ala Leu Val Ser Lys Gln Gly Gly Ile Leu Asn Asp Gln Leu Lys  
 325 330 335

Gln Ala Glu Phe Ile Phe His Asn Val Val Thr Thr Gly Leu Glu Val  
 340 345 350

Gln Lys Asp Ile Tyr Ser Gly Leu Ile Trp Leu His Ser Cys Gln Asp  
 355 360 365

Glu Val Asp Ile Gly Arg Ile Asn Ser Leu Arg Glu Glu Met Lys Lys  
 370 375 380

Ala Gly Phe Gln Glu Ser Lys Glu Val Val Val Ser Leu Leu Arg Ala  
 385 390 395 400

Tyr Ala Lys Glu Gly Gly Val Glu Glu Val Glu Arg Thr Trp Leu Glu  
 405 410 415

Leu Leu Asp Leu Asp Cys Gly Ile Pro Ser Gln Ala Phe Val Tyr Lys  
 420 425 430

Ile Glu Ala Tyr Ser Lys Val Gly Asp Phe Ala Lys Ala Met Glu Ile  
 435 440 445

Phe Arg Glu Met Glu Lys His Ile Gly Gly Ala Thr Met Ser Gly Tyr  
 450 455 460

His Lys Ile Ile Glu Val Leu Cys Lys Val Gln Gln Val Glu Leu Val  
 465 470 475 480

Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu  
 485 490 495

Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His  
 500 505 510

Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro  
 515 520 525

Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly  
 530 535 540

Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly  
 545 550 555 560

Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr  
 565 570 575

Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met  
 580 585 590

Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp  
 595 600 605

Tyr Ile Leu Ser Leu Lys Lys Lys Glu Val Lys Lys Arg Pro Phe Ser  
 610 615 620

Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu  
 625 630 635 640

Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile  
 645 650 655

Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln  
 660 665 670

Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe  
 675 680 685

Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr  
 690 695 700

Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile  
 705 710 715 720

Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp  
 725 730 735

Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg  
 740 745 750

Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln  
 755 760 765



Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Gly Lys Val Phe Trp  
 770 775 780

Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu  
 785 790 795 800

Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu  
 805 810 815

Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys  
 820 825 830

Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe  
 835 840 845

Tyr

<210> 9

<211> 1449

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1449)

<223> 8794

<400> 9

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atc gaa aaa ctc gac atc tta tct gac gac ttc gat cca acc gcc gta 96  
 Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val  
 20 25 30

gtc acc gaa ccg tta cct cct ccg gta act aat gga atc gga gct gat 144  
 Val Thr Glu Pro Leu Pro Pro Pro Val Thr Asn Gly Ile Gly Ala Asp  
 35 40 45

aaa gga gga gga gga gga gaa aga gag atg gtt ctc ggt agg aat ata 192  
 Lys Gly Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile  
 50 55 60

cac	aca	acg	tca	ctc	gct	gta	acg	gaa	ccg	gag	gtt	aac	gat	gaa	ttc	240
His	Thr	Thr	Ser	Leu	Ala	Val	Thr	Glu	Pro	Glu	Val	Asn	Asp	Glu	Phe	
65					70					75					80	
acc	gga	gat	aaa	gaa	gct	tat	atg	gct	agt	gtt	ctt	gct	cgt	tac	cgg	288
Thr	Gly	Asp	Lys	Glu	Ala	Tyr	Met	Ala	Ser	Val	Leu	Ala	Arg	Tyr	Arg	
				85					90					95		
aaa	act	ttg	gtt	gaa	cga	acc	aaa	aac	cat	tta	ggg	tat	cct	tat	aac	336
Lys	Thr	Leu	Val	Glu	Arg	Thr	Lys	Asn	His	Leu	Gly	Tyr	Pro	Tyr	Asn	
			100					105					110			
ttg	gat	ttc	gac	tat	ggg	gag	ctt	ggg	cag	tta	caa	cat	ttt	tcg	att	384
Leu	Asp	Phe	Asp	Tyr	Gly	Ala	Leu	Gly	Gln	Leu	Gln	His	Phe	Ser	Ile	
		115					120						125			
aat	aat	ctt	gga	gat	ccg	ttt	att	gaa	agt	aac	tat	ggg	gta	cac	tca	432
Asn	Asn	Leu	Gly	Asp	Pro	Phe	Ile	Glu	Ser	Asn	Tyr	Gly	Val	His	Ser	
	130					135					140					
aga	cct	ttt	gaa	gtt	ggg	gtg	ttg	gat	tgg	ttt	gct	cgt	ctt	tgg	gag	480
Arg	Pro	Phe	Glu	Val	Gly	Val	Leu	Asp	Trp	Phe	Ala	Arg	Leu	Trp	Glu	
145					150					155					160	
att	gag	aga	gat	gat	tat	tgg	ggg	tac	att	acc	aat	tgt	ggg	act	gaa	528
Ile	Glu	Arg	Asp	Asp	Tyr	Trp	Gly	Tyr	Ile	Thr	Asn	Cys	Gly	Thr	Glu	
			165					170						175		
ggc	aac	ctt	cat	ggc	att	tta	gtc	ggg	agg	gag	atg	ttt	ccg	gat	ggg	576
Gly	Asn	Leu	His	Gly	Ile	Leu	Val	Gly	Arg	Glu	Met	Phe	Pro	Asp	Gly	
		180						185					190			
ata	ttg	tat	gag	tcg	cgt	gaa	tcg	cat	tac	tcg	gtg	ttt	aaa	gct	gct	624
Ile	Leu	Tyr	Ala	Ser	Arg	Glu	Ser	His	Tyr	Ser	Val	Phe	Lys	Ala	Ala	
		195					200						205			
cga	atg	tat	cga	atg	gag	tgt	gag	aag	gtt	gat	acg	ctt	atg	tca	ggg	672
Arg	Met	Tyr	Arg	Met	Glu	Cys	Glu	Lys	Val	Asp	Thr	Leu	Met	Ser	Gly	
	210					215					220					
gag	att	gat	tgt	gat	gat	ttg	agg	aag	aag	ttg	ttg	gct	aat	aaa	gat	720
Glu	Ile	Asp	Cys	Asp	Asp	Leu	Arg	Lys	Lys	Leu	Leu	Ala	Asn	Lys	Asp	
225					230					235					240	
aaa	ccg	gag	att	ctt	aat	gtt	aac	ata	gga	acg	acg	gtt	aaa	gga	gct	768
Lys	Pro	Ala	Ile	Leu	Asn	Val	Asn	Ile	Gly	Thr	Thr	Val	Lys	Gly	Ala	
			245					250						255		
gtt	gat	gat	ctt	gac	ctt	gtt	atc	aaa	act	ctt	gaa	gag	tgt	ggg	ttc	816
Val	Asp	Asp	Leu	Asp	Leu	Val	Ile	Lys	Thr	Leu	Glu	Glu	Cys	Gly	Phe	
			260					265					270			
tca	cat	gat	agg	ttc	tat	att	cat	tgt	gat	gga	gct	ttg	ttt	gga	ctt	864
Ser	His	Asp	Arg	Phe	Tyr	Ile	His	Cys	Asp	Gly	Ala	Leu	Phe	Gly	Leu	
		275					280					285				
atg	atg	cct	ttt	gtc	aaa	cgt	gca	ccg	aaa	gtg	acg	ttt	aat	aaa	ccg	912
Met	Met	Pro	Phe	Val	Lys	Arg	Ala	Pro	Lys	Val	Thr	Phe	Asn	Lys	Pro	
	290					295					300					

ata ggg agt gtg agt gta tcg ggc cac aaa ttt gtc ggg tgt cca atg	960
Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met	
305 310 315 320	
cca tgt ggt gtt cag ata aca aga atg gaa cat atc aaa gtc ctc tcc	1008
Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser	
325 330 335	
agt aac gtt gag tac ctt gct tca agg gat gca aca atc atg gga agt	1056
Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser	
340 345 350	
cgt aac ggg cat gct cct ttg ttc ctc tgg tac acc tta aac agg aaa	1104
Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys	
355 360 365	
ggt tac aaa gga ttc cag aaa gaa gtt cag aaa tgc ttg aga aac gcg	1152
Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala	
370 375 380	
cat tac ctc aaa gac cga ctt cgt gaa gct ggg att agc gcc atg ctt	1200
His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu	
385 390 395 400	
aat gag ctt agc agc act gtg gtc ttt gaa cgg cct aaa gat gaa gag	1248
Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu	
405 410 415	
ttt gtt aga agg tgg cag ctt gct tgc caa ggt gat ata gct cat gtg	1296
Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val	
420 425 430	
gtg gtt atg cca agt gtt aca atc gag aag ctt gat aat ttc ctg aaa	1344
Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys	
435 440 445	
gac ctt gtc aaa cac aga ttg atc tgg tac gag gat gga tct cag cct	1392
Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro	
450 455 460	
cct tgc ctt gca tcg gag gta gga acc aac aac tgc atc tgt cca gct	1440
Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala	
465 470 475 480	
cac aag tga	1449
His Lys	

&lt;210&gt; 10

&lt;211&gt; 482

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 10

Met Val Gly Ser Leu Glu Ser Asp Gln Thr Leu Ser Met Ala Thr Leu  
 1 5 10 15

Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val  
 20 25 30

Val Thr Glu Pro Leu Pro Pro Pro Val Thr Asn Gly Ile Gly Ala Asp  
 35 40 45

Lys Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile  
 50 55 60

His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe  
 65 70 75 80

Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg  
 85 90 95

Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn  
 100 105 110

Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile  
 115 120 125

Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser  
 130 135 140

Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu  
 145 150 155 160

Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu  
 165 170 175

Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly  
 180 185 190

Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala  
 195 200 205

Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly  
 210 215 220

Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Leu Ala Asn Lys Asp  
 225 230 235 240

Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala  
 245 250 255  
 Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe  
 260 265 270  
 Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu  
 275 280 285  
 Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro  
 290 295 300  
 Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met  
 305 310 315 320  
 Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser  
 325 330 335  
 Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser  
 340 345 350  
 Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys  
 355 360 365  
 Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala  
 370 375 380  
 His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu  
 385 390 395 400  
 Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu  
 405 410 415  
 Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val  
 420 425 430  
 Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys  
 435 440 445  
 Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro  
 450 455 460  
 Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala  
 465 470 475 480

His Lys

&lt;210&gt; 11

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(483)

&lt;223&gt; 9106

&lt;400&gt; 11

atg gcg gaa cag act gag aaa gct ttt ctt aag cag cct aag gtc ttc	48
Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe	
1 5 10 15	

ctt agc tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga	96
Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly	
20 25 30	

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa	144
Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu	
35 40 45	

gcc att gat gga gct tac gtt gac aag aaa tgc ccc ttc act gga act	192
Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr	
50 55 60	

gtt tcc att aga ggt cgt atc tta gct ggt act tgc cac agt gcg aaa	240
Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys	
65 70 75 80	

atg cag agg acc att atc gtg cga agg gat tac ctt cac ttt gtg aag	288
Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys	
85 90 95	

aag tat cag agg tat gag aag agg cat tca aac att ccg gct cat gtc	336
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val	
100 105 110	

tca cca tgc ttc cgt gtt aag gaa gga gac cat atc atc att ggc caa	384
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln	
115 120 125	

tgc agg cca ttg tcg aag aca gtg agg ttc aat gtg ttg aag gtg ata	432
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Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Ile  
 130 135 140

cca gct ggg tct tct tct tca ttt gga aag aag gca ttc act gga atg 480  
 Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly Met  
 145 150 155 160

taa 483

<210> 12  
 <211> 160  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 12

Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe  
 1 5 10 15

Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly  
 20 25 30

Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
 35 40 45

Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr  
 50 55 60

Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys  
 65 70 75 80

Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys  
 85 90 95

Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val  
 100 105 110

Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln  
 115 120 125

Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Ile  
 130 135 140

Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly Met  
 145 150 155 160

&lt;210&gt; 13

&lt;211&gt; 1170

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1170)

&lt;223&gt; 10708

&lt;400&gt; 13

atg tct cac agg aag ttt gag cac cca aga cat ggt tct ctt ggt ttc	48
Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe	
1 5 10 15	
ctt cca agg aag aga gct aac cgt cac aga gga aag gtg aag gcg ttc	96
Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe	
20 25 30	
cct aag gat gac caa acc aag cct tgc aag ttc aca gct ttc atg ggt	144
Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly	
35 40 45	
tac aaa gct ggt atg act cac att gtc aga gaa gtg gag aaa cct gga	192
Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly	
50 55 60	
tcc aag ctt cac aag aag gag aca tgt gag gct gtt acc atc att gag	240
Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu	
65 70 75 80	
aca cct gct atg gtg gtt gtt gga gtt gtt gcc tat gtg aag act cct	288
Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro	
85 90 95	
aga ggt ttg agg tct ttg aac act gtc tgg gca cag cat ttg agt gag	336
Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu	
100 105 110	
gag gtc agg aga agg ttc tac aag aac tgg gct aag tct aag aag aag	384
Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys	
115 120 125	
gct ttc act ggg tac gct aag cag tat gac agt gag gat ggc aag aag	432
Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys	
130 135 140	
ggt att cag gct cag ctt gag aag atg aag aag tac gct act gtc atc	480



Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile	
145 150 155 160	
cgt gtt ttg gct cac act cag atc agg aag atg aag gga ttg aag cag	528
Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln	
165 170 175	
aag aag gct cac atg atg gag atc cag atc aat ggt ggt acc att gcc	576
Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala	
180 185 190	
cag aag gtt gac ttt gcc tac agt ttc ttt gag aag cag atc cca att	624
Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile	
195 200 205	
gaa gct gtc ttc cag aag gat gaa atg att gat atc att ggt gtg acc	672
Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr	
210 215 220	
aag ggt aag ggt tat gaa ggt gtt gtt act cgt tgg ggt gtt acc cgt	720
Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg	
225 230 235 240	
ctt cct cgt aag act cac aga ggt ctg cgt aag gtt gct tgt att ggt	768
Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly	
245 250 255	
gcg tgg cat cct gct aga gtg tcc tac act gtt gct agg gct ggt cag	816
Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln	
260 265 270	
aac ggt tac cat cac cgt act gag ctt aac aag aag att tac agg ttg	864
Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu	
275 280 285	
ggt aag gtt ggt act gag gca cac aca gcc atg act gaa tat gac agg	912
Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg	
290 295 300	
act gag aag gat gtg act cca atg gga ggc ttc cca cac tac ggt att	960
Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile	
305 310 315 320	
gtg aag gat gac tac ttg atg att aag ggg tgc tgt gtt ggt ccc aag	1008
Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys	
325 330 335	
aag aga gtt gta act ctc aga cag tca ctt ctc act cag act tcc cgt	1056
Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg	
340 345 350	
ctt gcc ttg gag gag atc aaa ctc aag ttt att gac acc gcc tcc att	1104
Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile	
355 360 365	
ttt gga cat ggt cgc ttc cag acc tcc ctt gag aag atg agg ttt tac	1152
Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr	
370 375 380	
aac cgt gtc acg aag taa	1170

Asn Arg Val Thr Lys  
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<210> 14

<211> 389

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe  
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Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe  
20 25 30

Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly  
35 40 45

Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly  
50 55 60

Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu  
65 70 75 80

Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro  
85 90 95

Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu  
100 105 110

Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys  
115 120 125

Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys  
130 135 140

Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile  
145 150 155 160

Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln  
165 170 175

Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala  
 180 185 190

Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile  
 195 200 205

Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr  
 210 215 220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg  
 225 230 235 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly  
 245 250 255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln  
 260 265 270

Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu  
 275 280 285

Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg  
 290 295 300

Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile  
 305 310 315 320

Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys  
 325 330 335

Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg  
 340 345 350

Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile  
 355 360 365

Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr  
 370 375 380

Asn Arg Val Thr Lys  
 385

<210> 15

<211> 351

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(351)

&lt;223&gt; 10844

&lt;400&gt; 15

atg aag cca gtg ata ggc aca gtg gta tcg aac aag atg caa aaa tct	48
Met Lys Pro Val Ile Gly Thr Val Val Ser Asn Lys Met Gln Lys Ser	
1 5 10 15	

gta gtg gtc gcc gtc gat aga ctc ttc cac aac aaa atc tac aat cgc	96
Val Val Val Ala Val Asp Arg Leu Phe His Asn Lys Ile Tyr Asn Arg	
20 25 30	

tac gtc aaa cga act tcc aaa ttc atg gct cac gac gac aaa gac gcc	144
Tyr Val Lys Arg Thr Ser Lys Phe Met Ala His Asp Asp Lys Asp Ala	
35 40 45	

tgc aac atc ggc gat cga gtg aag tta gat cca tca agg cct ttg agc	192
Cys Asn Ile Gly Asp Arg Val Lys Leu Asp Pro Ser Arg Pro Leu Ser	
50 55 60	

aag aat aag cat tgg att gtt gca gaa atc atc aaa aaa gct cga att	240
Lys Asn Lys His Trp Ile Val Ala Glu Ile Ile Lys Lys Ala Arg Ile	
65 70 75 80	

tat tct cct aaa gct gct gct gct gct gtt tct gct tct gct tct gct	288
Tyr Ser Pro Lys Ala Ala Ala Ala Ala Val Ser Ala Ser Ala Ser Ala	
85 90 95	

tcc tca gcc tcc act act gac tct tct gct cag tct cag att cct cca	336
Ser Ser Ala Ser Thr Thr Asp Ser Ser Ala Gln Ser Gln Ile Pro Pro	
100 105 110	

tca tct act tct taa	351
Ser Ser Thr Ser	
115	

&lt;210&gt; 16

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 16

Met Lys Pro Val Ile Gly Thr Val Val Ser Asn Lys Met Gln Lys Ser  
 1 5 10 15

Val Val Val Ala Val Asp Arg Leu Phe His Asn Lys Ile Tyr Asn Arg  
 20 25 30

Tyr Val Lys Arg Thr Ser Lys Phe Met Ala His Asp Asp Lys Asp Ala  
 35 40 45

Cys Asn Ile Gly Asp Arg Val Lys Leu Asp Pro Ser Arg Pro Leu Ser  
 50 55 60

Lys Asn Lys His Trp Ile Val Ala Glu Ile Ile Lys Lys Ala Arg Ile  
 65 70 75 80

Tyr Ser Pro Lys Ala Ala Ala Ala Ala Val Ser Ala Ser Ala Ser Ala  
 85 90 95

Ser Ser Ala Ser Thr Thr Asp Ser Ser Ala Gln Ser Gln Ile Pro Pro  
 100 105 110

Ser Ser Thr Ser  
 115

&lt;210&gt; 17

&lt;211&gt; 1269

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1269)

&lt;223&gt; 10951

&lt;400&gt; 17

atg tct tct tct gta gca gtg tta tgg gtt gct act tct tct cta aat 48  
 Met Ser Ser Ser Val Ala Val Leu Trp Val Ala Thr Ser Ser Leu Asn  
 1 5 10 15

cca gac cca atg aac aat tgt ggg ttg gta agg gtt cta gaa tct tct 96  
 Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser

20						25						30						
aga	ctg	ttc	tct	cct	tgt	cag	aat	cag	aga	cta	aac	aaa	ggg	aag	aag	144		
Arg	Leu	Phe	Ser	Pro	Cys	Gln	Asn	Gln	Arg	Leu	Asn	Lys	Gly	Lys	Lys			
		35					40					45						
aag	cag	ata	cca	act	tgg	agt	tct	tct	ttt	gta	agg	aac	cga	agt	aga	192		
Lys	Gln	Ile	Pro	Thr	Trp	Ser	Ser	Ser	Phe	Val	Arg	Asn	Arg	Ser	Arg			
	50					55					60							
aga	att	ggg	gtt	gtg	tct	tca	agc	tta	gta	gca	agt	cct	tct	gga	gag	240		
Arg	Ile	Gly	Val	Val	Ser	Ser	Ser	Leu	Val	Ala	Ser	Pro	Ser	Gly	Glu			
65					70					75					80			
ata	gct	ctt	tca	tct	gaa	gag	aag	gtt	tac	aat	gtt	gtg	ttg	aaa	caa	288		
Ile	Ala	Leu	Ser	Ser	Glu	Glu	Lys	Val	Tyr	Asn	Val	Val	Leu	Lys	Gln			
				85					90					95				
gct	gct	ttg	gtg	aac	aaa	cag	cta	agg	tct	tct	tct	tat	gac	ctt	gat	336		
Ala	Ala	Leu	Val	Asn	Lys	Gln	Leu	Arg	Ser	Ser	Ser	Tyr	Asp	Leu	Asp			
			100					105					110					
gtg	aag	aaa	cca	caa	gat	gtt	gtt	ctt	cct	ggg	agt	ttg	agt	ttg	ttg	384		
Val	Lys	Lys	Pro	Gln	Asp	Val	Val	Leu	Pro	Gly	Ser	Leu	Ser	Leu	Leu			
		115					120					125						
ggg	gaa	gct	tat	gat	cga	tgc	ggg	gaa	gtt	tgc	gct	gaa	tat	cct	aag	432		
Gly	Glu	Ala	Tyr	Asp	Arg	Cys	Gly	Glu	Val	Cys	Ala	Glu	Tyr	Pro	Lys			
	130					135					140							
acg	ttt	tat	ctt	gga	act	ttg	ctt	atg	aca	ccc	gaa	agg	cga	aag	gcg	480		
Thr	Phe	Tyr	Leu	Gly	Thr	Leu	Leu	Met	Thr	Pro	Glu	Arg	Arg	Lys	Ala			
145					150					155					160			
att	tgg	gca	atc	tac	gtt	tgg	tgt	aga	aga	act	gat	gaa	ctt	gtg	gat	528		
Ile	Trp	Ala	Ile	Tyr	Val	Trp	Cys	Arg	Arg	Thr	Asp	Glu	Leu	Val	Asp			
				165					170					175				
ggg	cca	aat	gct	tca	cat	ata	act	ccc	atg	gct	tta	gat	aga	tgg	gaa	576		
Gly	Pro	Asn	Ala	Ser	His	Ile	Thr	Pro	Met	Ala	Leu	Asp	Arg	Trp	Glu			
			180					185					190					
gca	agg	tta	gaa	gat	ctt	ttc	cgt	ggg	cgt	cct	ttc	gat	atg	ctt	gat	624		
Ala	Arg	Leu	Glu	Asp	Leu	Phe	Arg	Gly	Arg	Pro	Phe	Asp	Met	Leu	Asp			
		195					200					205						
gct	gct	ctc	gct	gat	aca	gtt	gct	aga	tac	ccg	gtc	gat	att	cag	cca	672		
Ala	Ala	Leu	Ala	Asp	Thr	Val	Ala	Arg	Tyr	Pro	Val	Asp	Ile	Gln	Pro			
	210					215					220							
ttt	cga	gac	atg	atc	gaa	gga	atg	aga	atg	gac	ttg	aag	aaa	tcg	aga	720		
Phe	Arg	Asp	Met	Ile	Glu	Gly	Met	Arg	Met	Asp	Leu	Lys	Lys	Ser	Arg			
225					230					235					240			
tac	cag	aac	ttc	gat	gat	cta	tac	ctt	tac	tgc	tac	tac	gtc	gct	gga	768		
Tyr	Gln	Asn	Phe	Asp	Asp	Leu	Tyr	Leu	Tyr	Cys	Tyr	Tyr	Val	Ala	Gly			
				245					250					255				
acc	gtc	gga	ttg	atg	agc	gtt	ccg	gtt	atg	gga	atc	gat	cct	aag	tcg	816		
Thr	Val	Gly	Leu	Met	Ser	Val	Pro	Val	Met	Gly	Ile	Asp	Pro	Lys	Ser			

260	265	270	
aaa gca aca acc gaa agt gtt tac aac gct gcc ttg gcc ctt ggt ata			864
Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile			
275	280	285	
gcc aat cag ctt act aac ata ctc aga gac gta ggc gaa gat gcg aga			912
Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg			
290	295	300	
aga gga agg gtt tat ctg cct cag gat gaa ttg gct cag gct ggt ctt			960
Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu			
305	310	315	320
tca gat gaa gac ata ttc gcc gga aaa gta act gat aaa tgg aga aac			1008
Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn			
325	330	335	
ttc atg aaa atg cag ctt aaa cga gca aga atg ttc ttc gac gaa gct			1056
Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala			
340	345	350	
gag aaa ggc gtc acc gag ctc agt gcc gct agc aga tgg cct gta tgg			1104
Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp			
355	360	365	
gct tca ttg cta ttg tac agg aga ata ctg gac gag att gaa gcg aat			1152
Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn			
370	375	380	
gat tac aac aat ttt act aag aga gct tat gtg ggg aaa gtc aag aaa			1200
Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys			
385	390	395	400
att gca gct ttg cca ttg gct tat gct aaa tca gta cta aag act tca			1248
Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser			
405	410	415	
agt tca aga cta tcg ata tga			1269
Ser Ser Arg Leu Ser Ile			
420			

&lt;210&gt; 18

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 18

Met	Ser	Ser	Ser	Val	Ala	Val	Leu	Trp	Val	Ala	Thr	Ser	Ser	Leu	Asn
1				5					10					15	

Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser

20					25					30					
Arg	Leu	Phe	Ser	Pro	Cys	Gln	Asn	Gln	Arg	Leu	Asn	Lys	Gly	Lys	Lys
		35					40					45			
Lys	Gln	Ile	Pro	Thr	Trp	Ser	Ser	Ser	Phe	Val	Arg	Asn	Arg	Ser	Arg
	50					55					60				
Arg	Ile	Gly	Val	Val	Ser	Ser	Ser	Leu	Val	Ala	Ser	Pro	Ser	Gly	Glu
65					70					75					80
Ile	Ala	Leu	Ser	Ser	Glu	Glu	Lys	Val	Tyr	Asn	Val	Val	Leu	Lys	Gln
				85					90					95	
Ala	Ala	Leu	Val	Asn	Lys	Gln	Leu	Arg	Ser	Ser	Ser	Tyr	Asp	Leu	Asp
			100					105					110		
Val	Lys	Lys	Pro	Gln	Asp	Val	Val	Leu	Pro	Gly	Ser	Leu	Ser	Leu	Leu
		115					120					125			
Gly	Glu	Ala	Tyr	Asp	Arg	Cys	Gly	Glu	Val	Cys	Ala	Glu	Tyr	Pro	Lys
	130					135					140				
Thr	Phe	Tyr	Leu	Gly	Thr	Leu	Leu	Met	Thr	Pro	Glu	Arg	Arg	Lys	Ala
145					150					155					160
Ile	Trp	Ala	Ile	Tyr	Val	Trp	Cys	Arg	Arg	Thr	Asp	Glu	Leu	Val	Asp
				165					170					175	
Gly	Pro	Asn	Ala	Ser	His	Ile	Thr	Pro	Met	Ala	Leu	Asp	Arg	Trp	Glu
			180					185					190		
Ala	Arg	Leu	Glu	Asp	Leu	Phe	Arg	Gly	Arg	Pro	Phe	Asp	Met	Leu	Asp
		195					200					205			
Ala	Ala	Leu	Ala	Asp	Thr	Val	Ala	Arg	Tyr	Pro	Val	Asp	Ile	Gln	Pro
	210					215					220				
Phe	Arg	Asp	Met	Ile	Glu	Gly	Met	Arg	Met	Asp	Leu	Lys	Lys	Ser	Arg
225					230					235					240
Tyr	Gln	Asn	Phe	Asp	Asp	Leu	Tyr	Leu	Tyr	Cys	Tyr	Tyr	Val	Ala	Gly
				245					250					255	
Thr	Val	Gly	Leu	Met	Ser	Val	Pro	Val	Met	Gly	Ile	Asp	Pro	Lys	Ser



260	265	270
Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile 275 280 285		
Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg 290 295 300		
Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu 305 310 315 320		
Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn 325 330 335		
Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala 340 345 350		
Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp 355 360 365		
Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn 370 375 380		
Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys 385 390 395 400		
Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser 405 410 415		
Ser Ser Arg Leu Ser Ile 420		

&lt;210&gt; 19

&lt;211&gt; 1125

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1125)

&lt;223&gt; 12935

&lt;400&gt; 19

atg gga gca gcg aag aat atc tgg gca tta gcc aac gcc gaa gat gca	48
Met Gly Ala Ala Lys Asn Ile Trp Ala Leu Ala Asn Ala Glu Asp Ala	
1 5 10 15	
gct aac gac gcc gaa caa atc cct tat tct tcg ttc gtc gtc gac acg	96
Ala Asn Asp Ala Glu Gln Ile Pro Tyr Ser Ser Phe Val Val Asp Thr	
20 25 30	
tct ttg cct ctt cct ctc atg att cct cgt atc ata gag tta tgt aaa	144
Ser Leu Pro Leu Pro Leu Met Ile Pro Arg Ile Ile Glu Leu Cys Lys	
35 40 45	
gat ctg ttc aag aat tgg gga gag ctt gat gat tca ctc ttc tct gtt	192
Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val	
50 55 60	
gag aga gta tct gga ggc att aca aat ctt ttg ctg aag gtt tct gtg	240
Glu Arg Val Ser Gly Gly Ile Thr Asn Leu Leu Leu Lys Val Ser Val	
65 70 75 80	
aaa gag gac act aat aaa gaa gtg tct gtt aca gtg aga ctg tat ggg	288
Lys Glu Asp Thr Asn Lys Glu Val Ser Val Thr Val Arg Leu Tyr Gly	
85 90 95	
cct aac act gag tat gtt att aac cgg gag aga gag att ctg gct atc	336
Pro Asn Thr Glu Tyr Val Ile Asn Arg Glu Arg Glu Ile Leu Ala Ile	
100 105 110	
aag tat ctc tcg gct gcc gga ttt ggt gcc aag ttg ctt ggt ggt ttt	384
Lys Tyr Leu Ser Ala Ala Gly Phe Gly Ala Lys Leu Leu Gly Gly Phe	
115 120 125	
gga aat ggc atg gtg caa tcg ttc atc aat gca aga acc tta gag cca	432
Gly Asn Gly Met Val Gln Ser Phe Ile Asn Ala Arg Thr Leu Glu Pro	
130 135 140	
tca gac atg aga gag cca aag att gct gca caa att gcc aga gaa ctt	480
Ser Asp Met Arg Glu Pro Lys Ile Ala Ala Gln Ile Ala Arg Glu Leu	
145 150 155 160	
gga aag ttt cat aaa gtg gac ata cca ggt tcc aag gaa cct cag ctg	528
Gly Lys Phe His Lys Val Asp Ile Pro Gly Ser Lys Glu Pro Gln Leu	
165 170 175	
tgg gtt gat atc ttg aag ttc tat gaa aaa gca tct act ctt acg ttt	576
Trp Val Asp Ile Leu Lys Phe Tyr Glu Lys Ala Ser Thr Leu Thr Phe	
180 185 190	
gaa gaa cct gat aag cag aag ctc ttt gag act att tcg ttt gaa gaa	624
Glu Glu Pro Asp Lys Gln Lys Leu Phe Glu Thr Ile Ser Phe Glu Glu	
195 200 205	
ctc cac aaa gaa att att gag cta agg gaa ttc aca ggc tta ctt aac	672
Leu His Lys Glu Ile Ile Glu Leu Arg Glu Phe Thr Gly Leu Leu Asn	
210 215 220	

gca cct gtg gtg ttt gct cat aac gat tta cta tca gga aac ttc atg 720  
 Ala Pro Val Val Phe Ala His Asn Asp Leu Leu Ser Gly Asn Phe Met  
 225 230 235 240  
  
 ctg aat gat gaa gaa gag aaa cta tac ttg att gat ttc gag tat gga 768  
 Leu Asn Asp Glu Glu Glu Lys Leu Tyr Leu Ile Asp Phe Glu Tyr Gly  
 245 250 255  
  
 tca tac aac tat aga ggc ttt gac atc gga aat cac ttc aat gaa tat 816  
 Ser Tyr Asn Tyr Arg Gly Phe Asp Ile Gly Asn His Phe Asn Glu Tyr  
 260 265 270  
  
 gca gga tac gac tgt gat tac agc ctg tac cca agt aaa gag gaa caa 864  
 Ala Gly Tyr Asp Cys Asp Tyr Ser Leu Tyr Pro Ser Lys Glu Glu Gln  
 275 280 285  
  
 tat cat ttc atc aag cat tac tta cag cca gac aaa cca gac gag gtc 912  
 Tyr His Phe Ile Lys His Tyr Leu Gln Pro Asp Lys Pro Asp Glu Val  
 290 295 300  
  
 agt atc gct gaa gta gaa tca gtc ttt gta gag aca gat gcg tat aaa 960  
 Ser Ile Ala Glu Val Glu Ser Val Phe Val Glu Thr Asp Ala Tyr Lys  
 305 310 315 320  
  
 tta gca tct cat ttg tac tgg gca ata tgg gcg atc atc cag gca agg 1008  
 Leu Ala Ser His Leu Tyr Trp Ala Ile Trp Ala Ile Ile Gln Ala Arg  
 325 330 335  
  
 atg tct ccc att gag ttt gaa tat ttg ggt tac ttc ttt ttg cgg tac 1056  
 Met Ser Pro Ile Glu Phe Glu Tyr Leu Gly Tyr Phe Phe Leu Arg Tyr  
 340 345 350  
  
 aat gaa tac aag aag cag aag cca ctt act ttt tca ctt gtt aca tct 1104  
 Asn Glu Tyr Lys Lys Gln Lys Pro Leu Thr Phe Ser Leu Val Thr Ser  
 355 360 365  
  
 cac ctc tca gca tcg ctg tag 1125  
 His Leu Ser Ala Ser Leu  
 370

&lt;210&gt; 20

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 20

Met Gly Ala Ala Lys Asn Ile Trp Ala Leu Ala Asn Ala Glu Asp Ala  
 1 5 10 15  
  
 Ala Asn Asp Ala Glu Gln Ile Pro Tyr Ser Ser Phe Val Val Asp Thr  
 20 25 30

Ser Leu Pro Leu Pro Leu Met Ile Pro Arg Ile Ile Glu Leu Cys Lys  
 35 40 45

Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val  
 50 55 60

Glu Arg Val Ser Gly Gly Ile Thr Asn Leu Leu Leu Lys Val Ser Val  
 65 70 75 80

Lys Glu Asp Thr Asn Lys Glu Val Ser Val Thr Val Arg Leu Tyr Gly  
 85 90 95

Pro Asn Thr Glu Tyr Val Ile Asn Arg Glu Arg Glu Ile Leu Ala Ile  
 100 105 110

Lys Tyr Leu Ser Ala Ala Gly Phe Gly Ala Lys Leu Leu Gly Gly Phe  
 115 120 125

Gly Asn Gly Met Val Gln Ser Phe Ile Asn Ala Arg Thr Leu Glu Pro  
 130 135 140

Ser Asp Met Arg Glu Pro Lys Ile Ala Ala Gln Ile Ala Arg Glu Leu  
 145 150 155 160

Gly Lys Phe His Lys Val Asp Ile Pro Gly Ser Lys Glu Pro Gln Leu  
 165 170 175

Trp Val Asp Ile Leu Lys Phe Tyr Glu Lys Ala Ser Thr Leu Thr Phe  
 180 185 190

Glu Glu Pro Asp Lys Gln Lys Leu Phe Glu Thr Ile Ser Phe Glu Glu  
 195 200 205

Leu His Lys Glu Ile Ile Glu Leu Arg Glu Phe Thr Gly Leu Leu Asn  
 210 215 220

Ala Pro Val Val Phe Ala His Asn Asp Leu Leu Ser Gly Asn Phe Met  
 225 230 235 240

Leu Asn Asp Glu Glu Glu Lys Leu Tyr Leu Ile Asp Phe Glu Tyr Gly  
 245 250 255

Ser Tyr Asn Tyr Arg Gly Phe Asp Ile Gly Asn His Phe Asn Glu Tyr  
 260 265 270

Ala Gly Tyr Asp Cys Asp Tyr Ser Leu Tyr Pro Ser Lys Glu Glu Gln  
 275 280 285

Tyr His Phe Ile Lys His Tyr Leu Gln Pro Asp Lys Pro Asp Glu Val  
 290 295 300

Ser Ile Ala Glu Val Glu Ser Val Phe Val Glu Thr Asp Ala Tyr Lys  
 305 310 315 320

Leu Ala Ser His Leu Tyr Trp Ala Ile Trp Ala Ile Ile Gln Ala Arg  
 325 330 335

Met Ser Pro Ile Glu Phe Glu Tyr Leu Gly Tyr Phe Phe Leu Arg Tyr  
 340 345 350

Asn Glu Tyr Lys Lys Gln Lys Pro Leu Thr Phe Ser Leu Val Thr Ser  
 355 360 365

His Leu Ser Ala Ser Leu  
 370

<210> 21

<211> 2283

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (2283)

<223> 13823

<400> 21

atg gcg atg act ccg gtc gcg tca tca tct cca gtt tca acc tgc aga 48  
 Met Ala Met Thr Pro Val Ala Ser Ser Ser Pro Val Ser Thr Cys Arg  
 1 5 10 15

ctc ttt cgc tgc aat ctc ctc cct gat ctc tta cct aag cct ctg ttt 96  
 Leu Phe Arg Cys Asn Leu Leu Pro Asp Leu Leu Pro Lys Pro Leu Phe  
 20 25 30

ctc tcc ctc ccc aaa cga aac aga att gcc tcg tgc cgc ttc act gta 144

Leu	Ser	Leu	Pro	Lys	Arg	Asn	Arg	Ile	Ala	Ser	Cys	Arg	Phe	Thr	Val	
		35					40				45					
cgt	gcc	tcc	gcg	aat	gct	acc	gtc	gaa	tcc	cct	aac	ggg	gtc	cct	gcc	192
Arg	Ala	Ser	Ala	Asn	Ala	Thr	Val	Glu	Ser	Pro	Asn	Gly	Val	Pro	Ala	
	50					55				60						
tcc	aca	tca	gat	acg	gat	acg	gag	acg	gat	acc	acc	tcc	tat	ggc	cga	240
Ser	Thr	Ser	Asp	Thr	Asp	Thr	Glu	Thr	Asp	Thr	Thr	Ser	Tyr	Gly	Arg	
65					70				75					80		
cag	ttt	ttc	cct	ttg	gcc	gca	gtt	gtt	ggc	cag	gaa	ggc	ata	aaa	act	288
Gln	Phe	Phe	Pro	Leu	Ala	Ala	Val	Val	Gly	Gln	Glu	Gly	Ile	Lys	Thr	
				85				90					95			
gct	ctt	tta	ctt	ggc	gcg	gtt	gat	cgt	gaa	atc	gga	ggg	att	gcc	att	336
Ala	Leu	Leu	Leu	Gly	Ala	Val	Asp	Arg	Glu	Ile	Gly	Gly	Ile	Ala	Ile	
			100					105					110			
tca	ggg	cgt	aga	ggc	act	gca	aaa	aca	gtc	atg	gcg	cga	ggg	ctt	cat	384
Ser	Gly	Arg	Arg	Gly	Thr	Ala	Lys	Thr	Val	Met	Ala	Arg	Gly	Leu	His	
		115					120					125				
gaa	atc	ctc	cct	cct	att	gaa	gtt	gtt	gta	ggc	tca	ata	tca	aat	gct	432
Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val	Gly	Ser	Ile	Ser	Asn	Ala	
	130					135				140						
gac	cca	gct	tgt	cca	gat	gag	tgg	gaa	gat	gac	tta	gat	gag	cgc	ata	480
Asp	Pro	Ala	Cys	Pro	Asp	Glu	Trp	Glu	Asp	Asp	Leu	Asp	Glu	Arg	Ile	
145					150				155					160		
gag	tac	aat	gct	gac	aat	acc	att	aag	act	gag	att	gtc	aaa	tct	cct	528
Glu	Tyr	Asn	Ala	Asp	Asn	Thr	Ile	Lys	Thr	Glu	Ile	Val	Lys	Ser	Pro	
				165				170					175			
ttc	att	cag	att	cca	cta	gga	gtt	aca	gaa	gac	aga	ctc	att	ggg	tct	576
Phe	Ile	Gln	Ile	Pro	Leu	Gly	Val	Thr	Glu	Asp	Arg	Leu	Ile	Gly	Ser	
			180					185					190			
gtt	gat	gtt	gag	gag	tct	gtg	aaa	agg	ggg	aca	act	gtt	ttc	caa	cct	624
Val	Asp	Val	Glu	Glu	Ser	Val	Lys	Arg	Gly	Thr	Thr	Val	Phe	Gln	Pro	
		195				200						205				
ggg	ctt	ttg	gct	gaa	gcc	cat	aga	gga	gtg	ttg	tat	gtt	gat	gaa	ata	672
Gly	Leu	Leu	Ala	Glu	Ala	His	Arg	Gly	Val	Leu	Tyr	Val	Asp	Glu	Ile	
	210					215					220					
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Asn	Leu	Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu	Leu	Leu	Asn	Val	Leu	Thr	
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gat	ggg	gtt	aat	ata	gtt	gaa	aga	gaa	gga	atc	agc	ttt	agg	cac	ccg	768
Asp	Gly	Val	Asn	Ile	Val	Glu	Arg	Glu	Gly	Ile	Ser	Phe	Arg	His	Pro	
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tgc	aaa	cca	ctt	tta	att	gca	acc	tat	aac	cct	gaa	gaa	ggg	gct	gtt	816
Cys	Lys	Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn	Pro	Glu	Glu	Gly	Ala	Val	
			260					265					270			
cga	gag	cac	ttg	cta	gac	cgt	gtt	gcc	att	aat	tta	agt	gca	gac	cta	864

Arg	Glu	His	Leu	Leu	Asp	Arg	Val	Ala	Ile	Asn	Leu	Ser	Ala	Asp	Leu		
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cct	atg	agt	ttt	gaa	gat	cgt	gtc	gca	gca	gtt	gga	att	gcc	aca	cag		912
Pro	Met	Ser	Phe	Glu	Asp	Arg	Val	Ala	Ala	Val	Gly	Ile	Ala	Thr	Gln		
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Phe	Gln	Glu	Arg	Cys	Asn	Glu	Val	Phe	Arg	Met	Val	Asn	Glu	Glu	Thr		
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gaa	aca	gca	aag	acg	cag	att	ata	ttg	gct	aga	gaa	tat	ttg	aaa	gat		1008
Glu	Thr	Ala	Lys	Thr	Gln	Ile	Ile	Leu	Ala	Arg	Glu	Tyr	Leu	Lys	Asp		
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gtc	aag	ata	agt	aga	gag	caa	ttg	aag	tat	ctg	gtt	ttg	gaa	gct	gtc		1056
Val	Lys	Ile	Ser	Arg	Glu	Gln	Leu	Lys	Tyr	Leu	Val	Leu	Glu	Ala	Val		
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cga	ggg	ggg	gtc	cag	gga	cac	cgc	gcc	gaa	ttg	tat	gca	gct	cgt	gtg		1104
Arg	Gly	Gly	Val	Gln	Gly	His	Arg	Ala	Glu	Leu	Tyr	Ala	Ala	Arg	Val		
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gcg	aag	tgt	tta	gct	gca	att	gaa	gga	cga	gaa	aaa	gtc	aca	atc	gat		1152
Ala	Lys	Cys	Leu	Ala	Ala	Ile	Glu	Gly	Arg	Glu	Lys	Val	Thr	Ile	Asp		
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Asp	Leu	Arg	Lys	Ala	Val	Glu	Leu	Val	Ile	Leu	Pro	Arg	Ser	Ser	Leu		
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Asp	Glu	Thr	Pro	Pro	Glu	Gln	Gln	Asn	Gln	Pro	Pro	Pro	Pro	Pro	Pro		
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cct	cca	caa	aat	agc	gaa	tct	gga	gaa	gaa	gaa	aat	gaa	gaa	gaa	caa		1296
Pro	Pro	Gln	Asn	Ser	Glu	Ser	Gly	Glu	Glu	Glu	Asn	Glu	Glu	Glu	Gln		
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gaa	gaa	gaa	gaa	gag	gat	gaa	agc	aat	gaa	gaa	aat	gaa	aat	gag	cag		1344
Glu	Glu	Glu	Glu	Glu	Asp	Glu	Ser	Asn	Glu	Glu	Asn	Glu	Asn	Glu	Gln		
		435				440						445					
caa	cag	gac	caa	ata	cct	gaa	gag	ttt	ata	ttt	gac	gct	gag	ggc	ggg		1392
Gln	Gln	Asp	Gln	Ile	Pro	Glu	Glu	Phe	Ile	Phe	Asp	Ala	Glu	Gly	Gly		
	450					455					460						
ctg	gtg	gat	gag	aaa	ctc	ctc	ttc	ttt	gct	caa	caa	gcc	cag	aaa	cgt		1440
Leu	Val	Asp	Glu	Lys	Leu	Leu	Phe	Phe	Ala	Gln	Gln	Ala	Gln	Lys	Arg		
	465				470				475						480		
cgg	ggg	aaa	gct	ggc	agg	gcg	aag	aat	gtc	ata	ttc	tca	gaa	gat	aga		1488
Arg	Gly	Lys	Ala	Gly	Arg	Ala	Lys	Asn	Val	Ile	Phe	Ser	Glu	Asp	Arg		
			485					490					495				
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Gly	Arg	Tyr	Ile	Lys	Pro	Met	Leu	Pro	Lys	Gly	Pro	Val	Lys	Arg	Leu		
			500					505					510				
gct	gtg	gat	gca	acc	ctt	aga	gca	gct	gca	cca	tac	cag	aaa	ttg	cgc		1584

Ala Val Asp	Ala Thr Leu Arg	Ala Ala Ala Pro Tyr Gln Lys Leu Arg	
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aga gag aag gat atc tca gga act agg aaa gtc ttt gtt gag aag aca			1632
Arg Glu Lys Asp Ile Ser Gly Thr Arg Lys Val Phe Val Glu Lys Thr			
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gat atg agg gcc aaa aga atg gca agg aaa gct gga gcc ctg gtt atc			1680
Asp Met Arg Ala Lys Arg Met Ala Arg Lys Ala Gly Ala Leu Val Ile			
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ttt gtg gtt gat gca agt ggc agt atg gca ttg aat cgt atg caa aac			1728
Phe Val Val Asp Ala Ser Gly Ser Met Ala Leu Asn Arg Met Gln Asn			
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gcc aaa ggt gct gca ctc aaa cta ctg gca gag agc tat act agc agg			1776
Ala Lys Gly Ala Ala Leu Lys Leu Leu Ala Glu Ser Tyr Thr Ser Arg			
580	585	590	
gat cag gtt tct att att cct ttc cga ggg gat gct gcg gaa gtg ctc			1824
Asp Gln Val Ser Ile Ile Pro Phe Arg Gly Asp Ala Ala Glu Val Leu			
595	600	605	
ttg ccc cct tct aga tca ata gca atg gca agg aat cgt ctt gag aga			1872
Leu Pro Pro Ser Arg Ser Ile Ala Met Ala Arg Asn Arg Leu Glu Arg			
610	615	620	
ctt cct tgt ggt ggt ggt tct cct ctt gcc cat ggt tta aca acg gct			1920
Leu Pro Cys Gly Gly Gly Ser Pro Leu Ala His Gly Leu Thr Thr Ala			
625	630	635	640
gta aga gta gga ctt aac gca gag aag agt ggt gat gtc ggg cgc ata			1968
Val Arg Val Gly Leu Asn Ala Glu Lys Ser Gly Asp Val Gly Arg Ile			
645	650	655	
atg att gtt gcg ata acc gat ggt cga gcc aac att aca ctg aaa aga			2016
Met Ile Val Ala Ile Thr Asp Gly Arg Ala Asn Ile Thr Leu Lys Arg			
660	665	670	
tca act gat ccg gag tct att gcc cca gat gct cct aga ccc acg tcc			2064
Ser Thr Asp Pro Glu Ser Ile Ala Pro Asp Ala Pro Arg Pro Thr Ser			
675	680	685	
aaa gaa ttg aag gat gag att ctg gaa gtt gct ggg aag ata tac aag			2112
Lys Glu Leu Lys Asp Glu Ile Leu Glu Val Ala Gly Lys Ile Tyr Lys			
690	695	700	
gca ggg atg tct ctt cta gtg att gat acc gag aac aag ttt gtt tca			2160
Ala Gly Met Ser Leu Leu Val Ile Asp Thr Glu Asn Lys Phe Val Ser			
705	710	715	720
act ggt ttt gca aag gag atc gca aga gtt gct caa gga aaa tat tat			2208
Thr Gly Phe Ala Lys Glu Ile Ala Arg Val Ala Gln Gly Lys Tyr Tyr			
725	730	735	
tac ttg cca aat gct tct gat gct gta atc tct gcc acc act agg gat			2256
Tyr Leu Pro Asn Ala Ser Asp Ala Val Ile Ser Ala Thr Thr Arg Asp			
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Ser Thr Ser Asp Thr Asp Thr Glu Thr Asp Thr Thr Ser Tyr Gly Arg  
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Gln Phe Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr  
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Ser Gly Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His  
115 120 125

Glu Ile Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala  
130 135 140

Asp Pro Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile  
145 150 155 160

Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro  
165 170 175

Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser  
 180 185 190

Val Asp Val Glu Glu Ser Val Lys Arg Gly Thr Thr Val Phe Gln Pro  
 195 200 205

Gly Leu Leu Ala Glu Ala His Arg Gly Val Leu Tyr Val Asp Glu Ile  
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Asn Leu Leu Asp Glu Gly Ile Ser Asn Leu Leu Leu Asn Val Leu Thr  
 225 230 235 240

Asp Gly Val Asn Ile Val Glu Arg Glu Gly Ile Ser Phe Arg His Pro  
 245 250 255

Cys Lys Pro Leu Leu Ile Ala Thr Tyr Asn Pro Glu Glu Gly Ala Val  
 260 265 270

Arg Glu His Leu Leu Asp Arg Val Ala Ile Asn Leu Ser Ala Asp Leu  
 275 280 285

Pro Met Ser Phe Glu Asp Arg Val Ala Ala Val Gly Ile Ala Thr Gln  
 290 295 300

Phe Gln Glu Arg Cys Asn Glu Val Phe Arg Met Val Asn Glu Glu Thr  
 305 310 315 320

Glu Thr Ala Lys Thr Gln Ile Ile Leu Ala Arg Glu Tyr Leu Lys Asp  
 325 330 335

Val Lys Ile Ser Arg Glu Gln Leu Lys Tyr Leu Val Leu Glu Ala Val  
 340 345 350

Arg Gly Gly Val Gln Gly His Arg Ala Glu Leu Tyr Ala Ala Arg Val  
 355 360 365

Ala Lys Cys Leu Ala Ala Ile Glu Gly Arg Glu Lys Val Thr Ile Asp  
 370 375 380

Asp Leu Arg Lys Ala Val Glu Leu Val Ile Leu Pro Arg Ser Ser Leu  
 385 390 395 400

Asp Glu Thr Pro Pro Glu Gln Gln Asn Gln Pro Pro Pro Pro Pro Pro  
 405 410 415

Pro Pro Gln Asn Ser Glu Ser Gly Glu Glu Glu Asn Glu Glu Glu Gln  
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Glu Glu Glu Glu Glu Asp Glu Ser Asn Glu Glu Asn Glu Asn Glu Gln  
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Gln Gln Asp Gln Ile Pro Glu Glu Phe Ile Phe Asp Ala Glu Gly Gly  
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Leu Val Asp Glu Lys Leu Leu Phe Phe Ala Gln Gln Ala Gln Lys Arg  
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Arg Gly Lys Ala Gly Arg Ala Lys Asn Val Ile Phe Ser Glu Asp Arg  
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Gly Arg Tyr Ile Lys Pro Met Leu Pro Lys Gly Pro Val Lys Arg Leu  
                     500                    505                    510

Ala Val Asp Ala Thr Leu Arg Ala Ala Ala Pro Tyr Gln Lys Leu Arg  
                     515                    520                    525

Arg Glu Lys Asp Ile Ser Gly Thr Arg Lys Val Phe Val Glu Lys Thr  
                     530                    535                    540

Asp Met Arg Ala Lys Arg Met Ala Arg Lys Ala Gly Ala Leu Val Ile  
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Phe Val Val Asp Ala Ser Gly Ser Met Ala Leu Asn Arg Met Gln Asn  
                     565                    570                    575

Ala Lys Gly Ala Ala Leu Lys Leu Leu Ala Glu Ser Tyr Thr Ser Arg  
                     580                    585                    590

Asp Gln Val Ser Ile Ile Pro Phe Arg Gly Asp Ala Ala Glu Val Leu  
                     595                    600                    605

Leu Pro Pro Ser Arg Ser Ile Ala Met Ala Arg Asn Arg Leu Glu Arg  
                     610                    615                    620

Leu Pro Cys Gly Gly Gly Ser Pro Leu Ala His Gly Leu Thr Thr Ala  
 625                    630                    635                    640

Val Arg Val Gly Leu Asn Ala Glu Lys Ser Gly Asp Val Gly Arg Ile  
                     645                    650                    655

Met Ile Val Ala Ile Thr Asp Gly Arg Ala Asn Ile Thr Leu Lys Arg  
                     660                    665                    670

Ser Thr Asp Pro Glu Ser Ile Ala Pro Asp Ala Pro Arg Pro Thr Ser  
                     675                    680                    685

Lys Glu Leu Lys Asp Glu Ile Leu Glu Val Ala Gly Lys Ile Tyr Lys  
                     690                    695                    700

Ala Gly Met Ser Leu Leu Val Ile Asp Thr Glu Asn Lys Phe Val Ser  
                     705                    710                    715                    720

Thr Gly Phe Ala Lys Glu Ile Ala Arg Val Ala Gln Gly Lys Tyr Tyr  
                     725                    730                    735

Tyr Leu Pro Asn Ala Ser Asp Ala Val Ile Ser Ala Thr Thr Arg Asp  
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 1                    5                    10                    15

att gct tca ttc act gga aat gga gaa gct tct tct tct tcc tca gag 96  
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                     20                    25                    30

aac aat ggc tgc aat gga gat caa aac cat ttg ctt aac gaa ctc aaa 144  
 Asn Asn Gly Cys Asn Gly Asp Gln Asn His Leu Leu Asn Glu Leu Lys  
                     35                    40                    45

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ttg ctt agc aag gaa gag aaa atc cga ggt ttg gag tta tat atc agg Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg 65 70 75 80	240
gag aaa cct tat ttg ttt gag agt gaa att gat ttt tct caa ttt gag Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu 85 90 95	288
aat ccg gta aag cat gcg agt gaa gta gaa gag aag gtt tat gaa cta Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu 100 105 110	336
cag aaa cag gta ttt gga tta aaa cgg gaa gtg gaa acg caa cgc aag Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys 115 120 125	384
aga agg ctc gaa gtg gaa gct gaa tta gca gat aag aaa gtt gca caa Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln 130 135 140	432
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ccg tac acg acc cgg att atg acc tta acg aag cca cac ttg gag aga Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg 275 280 285	864

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Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe  
290 295 300

cag aag ttg gtt aac tca acc aaa atc tac cat caa cag gct caa gaa 960  
Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu  
305 310 315 320

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325 330 335

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340 345 350

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Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu  
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Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln  
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                             165                            170                            175

Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met  
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Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu  
                             195                            200                            205

Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr  
                             210                            215                            220

Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu  
                             225                            230                            235                            240

Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly  
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Phe Asp Ala Ser Tyr Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His  
                             260                            265                            270

Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg  
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Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe  
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Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu  
                             305                            310                            315                            320

Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu  
325 330 335

Ala Trp Val Gly Ala Thr Ala Leu Ile Gly Phe Pro Leu Ile Phe Ile  
340 345 350

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Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His
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Ser	Thr	Ala	Glu	Asp	Ile	Val	Asp	Asp	Leu	Arg	Ser	Arg	Tyr	Gly	Asn	
		35					40					45				

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Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg	
85 90 95	
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Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His	
100 105 110	
tta agg aag agg aat atg gaa cgt tca gtg tct tct tct ccg tct tct	384
Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Ser Pro Ser Ser	
115 120 125	
tct tct tct tcg gaa gac agt ggt gat gtg tcg act tct gag gac gcg	432
Ser Ser Ser Ser Glu Asp Ser Gly Asp Val Ser Thr Ser Glu Asp Ala	
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Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp	
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Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro	
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Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn	
180 185 190	
aaa ggt aga agc aag ttg gct aca atg ggg gcc aga aag gag gct aaa	624
Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys	
195 200 205	
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Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val	
210 215 220	
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Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys	
225 230 235 240	
ata ttg gat gaa ttg gag atg aat gtt cta ttc ccc att ctc aat cct	768
Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro	
245 250 255	
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Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe	
260 265 270	
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His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala	
275 280 285	
aat gaa gct ggt gtt ccg ttt tat aag att tca gcc aca gag gtg att	912
Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile	
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Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser	
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Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp	
325 330 335	
gcg att ggt tca aag aga gag aat cag caa aga gag atg gag aag cgg	1056
Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg	
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Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly	
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Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly	
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Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly	
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Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg	
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Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro	
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Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg	
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Ile Leu Asp Ser Arg Lys Ser Glu Gln Ser Gly Asp Gly Glu Asp Asp	
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Lys Ser Trp Leu Arg Met Pro Trp Pro Glu Glu Glu Leu Glu Lys Leu	
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Phe Val Lys Met Ser Asp Phe Glu Glu Ala Val Asn Leu Val Gln Ala	
500 505 510	
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Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile	
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Leu	Glu	Thr	Gly	Phe 565	Leu	Leu	Tyr	Gly	Pro 570	Pro	Gly	Cys	Gly	Lys 575	Thr	
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Ala	Ile 610	Arg	Thr	Leu	Phe	Gln 615	Arg	Ala	Arg	Thr	Cys 620	Ala	Pro	Cys	Val	
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Gly	Ala	Trp	Val	Val 645	Glu	Arg	Leu	Leu	Asn 650	Gln	Phe	Leu	Val	Glu 655	Leu	
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cca	gat	gta	gtt	gat	cct	gct	ttc	ttg	aga	ccg	ggt	aga	ttt	ggg	aat	2064
Pro	Asp	Val	Val	Asp 675	Pro	Ala	Phe 680	Leu	Arg	Pro	Gly	Arg 685	Phe	Gly	Asn	
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Leu	Leu 690	Tyr	Val	Pro	Leu	Pro 695	Asn	Ala	Asp	Glu	Arg 700	Ala	Ser	Ile	Leu	
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Lys	Ala	Ile	Ala	Arg	Lys 710	Lys	Pro	Ile	Asp	Pro 715	Ser	Val	Asp	Leu	Asp 720	
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Gly	Ile	Ala	Lys 725	Asn	Asn	Cys	Glu	Gly	Phe 730	Ser	Gly	Ala	Asp	Leu 735	Ala	
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Ile	Lys 770	Thr	Arg	His	Phe	Glu	Gln 775	Ala	Leu	Ser	Leu	Val 780	Ser	Pro	Ser	
gtg	aac	aaa	cag	caa	aga	aga	cac	tat	gac	gca	cta	tca	aca	aag	ctt	2400

Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu  
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 Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Leu Asn Val Arg Gln Val  
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 Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His  
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Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp  
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Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro  
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Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn  
 180 185 190

Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys  
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Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val  
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Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys  
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Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro  
 245 250 255

Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe  
 260 265 270

His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala  
 275 280 285

Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile  
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Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser  
 305 310 315 320

Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp  
 325 330 335

Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg  
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Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly  
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Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly  
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Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly  
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Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg  
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Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro  
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Phe Asp Lys Lys Arg Ile Ala Arg Leu Thr Pro Gly Phe Val Gly Ala  
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Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg  
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Lys Ser Trp Leu Arg Met Pro Trp Pro Glu Glu Glu Leu Glu Lys Leu  
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Phe Val Lys Met Ser Asp Phe Glu Glu Ala Val Asn Leu Val Gln Ala  
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Ser Leu Thr Arg Glu Gly Phe Ser Ile Val Pro Asp Val Lys Trp Asp  
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Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile  
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Val Arg Pro Ile Lys Lys Pro Asp Ile Tyr Lys Ala Phe Gly Val Asp  
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Leu Ile Ala Lys Ala Ala Ala Asn Glu Ala Gly Ala Asn Phe Met His  
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Ile Lys Gly Ala Glu Leu Leu Asn Lys Tyr Val Gly Glu Ser Glu Leu  
 595 600 605

Ala Ile Arg Thr Leu Phe Gln Arg Ala Arg Thr Cys Ala Pro Cys Val  
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Ile Phe Phe Asp Glu Val Asp Ala Leu Thr Thr Ser Arg Gly Lys Glu  
625 630 635 640

Gly Ala Trp Val Val Glu Arg Leu Leu Asn Gln Phe Leu Val Glu Leu  
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Asp Gly Gly Glu Arg Arg Asn Val Tyr Val Ile Gly Ala Thr Asn Arg  
660 665 670

Pro Asp Val Val Asp Pro Ala Phe Leu Arg Pro Gly Arg Phe Gly Asn  
675 680 685

Leu Leu Tyr Val Pro Leu Pro Asn Ala Asp Glu Arg Ala Ser Ile Leu  
690 695 700

Lys Ala Ile Ala Arg Lys Lys Pro Ile Asp Pro Ser Val Asp Leu Asp  
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Gly Ile Ala Lys Asn Asn Cys Glu Gly Phe Ser Gly Ala Asp Leu Ala  
725 730 735

His Leu Val Gln Lys Ala Thr Phe Gln Ala Val Glu Glu Met Ile Gly  
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Ser Ser Glu Ser Ser Glu Asp Asp Val Thr Asp Ile Thr Gln Cys Thr  
755 760 765

Ile Lys Thr Arg His Phe Glu Gln Ala Leu Ser Leu Val Ser Pro Ser  
770 775 780

Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu  
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Gly	Phe	Asp	Asp	Pro	Ser	Ile	Asp	Lys	Met	Leu	Arg	Lys	Cys	Lys	Gln	
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Leu	Glu	Lys	Ala	Gln	Ser	Asp	Val	Ala	Ser	Glu	Asn	Trp	Asp	Tyr	Leu	
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Ser	Asn	Ile	Val	Gly	Ile	Gln	Glu	Arg	Lys	Leu	Pro	Tyr	Ile	Val	Ser	
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Met	Val	Glu	Cys	Leu	Ser	Ser	Leu	Gly	Arg	Asn	Pro	Arg	Glu	Val	Ala	
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tcc	gcc	att	acc	aaa	ttt	cct	cca	ata	ctc	tct	cat	agc	gtg	gag	gag	336
Ser	Ala	Ile	Thr	Lys	Phe	Pro	Pro	Ile	Leu	Ser	His	Ser	Val	Glu	Glu	
			100					105						110		

aaa	ctc	tgt	ccc	ctt	ctt	gct	ttc	ttt	caa	gcg	tta	ggt	gtg	cct	gag	384
Lys	Leu	Cys	Pro	Leu	Leu	Ala	Phe	Phe	Gln	Ala	Leu	Gly	Val	Pro	Glu	
		115					120						125			

act	caa	ctt	ggc	aaa	atg	ata	ctt	ttt	aac	cca	agg	ctt	atc	agc	tac	432
Thr	Gln	Leu	Gly	Lys	Met	Ile	Leu	Phe	Asn	Pro	Arg	Leu	Ile	Ser	Tyr	
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Ser	Ile	Asp	Thr	Lys	Leu	Thr	Val	Ile	Val	Ser	Phe	Leu	Ala	Ser	Leu	
145					150					155					160	

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Gly	Leu	Asp	Gln	Asp	Gly	Met	Ile	Gly	Lys	Val	Leu	Val	Lys	Asn	Pro	
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Phe	Leu	Met	Gly	Tyr	Ser	Val	Asp	Lys	Arg	Leu	Arg	Pro	Thr	Thr	Glu	
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Val Met Asn Phe Pro Gln Leu Leu Cys Arg Asp Val Asn Lys Ile Leu
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Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln
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ata gca acc atg gtc act ggt tat ccc caa atc ttg att aag agt gtt      768
Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val
      245                      250                      255

aag aat tca cta cag cct agg atc aga ttc ctc gtc cag gtg atg gga      816
Lys Asn Ser Leu Gln Pro Arg Ile Arg Phe Leu Val Gln Val Met Gly
      260                      265                      270

aga ggc atg gat gaa gtg gct tct tat cct gaa ttc ttt cac cat gga      864
Arg Gly Met Asp Glu Val Ala Ser Tyr Pro Glu Phe Phe His His Gly
      275                      280                      285

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Leu Lys Lys Lys Val Glu Ser Arg Phe Lys Leu Val Lys Lys Asn Asn
      290                      295                      300

att gac tgc agc ctt aga gaa atg ctg gac tgt aac aca aag aaa ttc      960
Ile Asp Cys Ser Leu Arg Glu Met Leu Asp Cys Asn Thr Lys Lys Phe
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cat gag aag ttt ggc ttt tcg gag gta act gca agc tcc tag      1002
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Gly Phe Asp Asp Pro Ser Ile Asp Lys Met Leu Arg Lys Cys Lys Gln
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Leu Glu Lys Ala Gln Ser Asp Val Ala Ser Glu Asn Trp Asp Tyr Leu
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Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro  
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Met Val Glu Cys Leu Ser Ser Leu Gly Arg Asn Pro Arg Glu Val Ala  
85 90 95

Ser Ala Ile Thr Lys Phe Pro Pro Ile Leu Ser His Ser Val Glu Glu  
100 105 110

Lys Leu Cys Pro Leu Leu Ala Phe Phe Gln Ala Leu Gly Val Pro Glu  
115 120 125

Thr Gln Leu Gly Lys Met Ile Leu Phe Asn Pro Arg Leu Ile Ser Tyr  
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Ser Ile Asp Thr Lys Leu Thr Val Ile Val Ser Phe Leu Ala Ser Leu  
145 150 155 160

Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro  
165 170 175

Phe Leu Met Gly Tyr Ser Val Asp Lys Arg Leu Arg Pro Thr Thr Glu  
180 185 190

Phe Leu Lys Ser Ser Val Gly Leu Ser Glu Asp Gly Ile Lys Ser Val  
195 200 205

Val Met Asn Phe Pro Gln Leu Leu Cys Arg Asp Val Asn Lys Ile Leu  
210 215 220

Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln  
225 230 235 240

Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val  
245 250 255

Lys Asn Ser Leu Gln Pro Arg Ile Arg Phe Leu Val Gln Val Met Gly  
260 265 270

Arg Gly Met Asp Glu Val Ala Ser Tyr Pro Glu Phe Phe His His Gly  
275 280 285

Leu Lys Lys Lys Val Glu Ser Arg Phe Lys Leu Val Lys Lys Asn Asn  
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Thr	His	Arg	Ile	Tyr	Lys	His	Glu	Cys	Cys	Ile	Ser	Phe	Asp	Thr	Pro	
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Arg	Ser	Glu	Gly	Gly	Leu	Phe	Val	Asp	Met	Asn	Ser	Phe	Leu	Ala	Phe	
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Tyr	Leu	His	Ile	Lys	Gln	Thr	Arg	Lys	Ser	Ile	Pro	Glu	Asp	Arg	Pro	
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Leu	Lys	Lys	Pro	Thr	Leu	Leu	Ala	Ile	Gly	Val	Asp	Gly	Gly	Phe	Asp	
				85					90					95		

aac	aat	gag	cca	gag	tac	gag	gag	tct	tat	agc	ata	gtc	ata	ctt	ccg	336
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Asp	Phe	Val	Ser	Leu	Pro	Phe	Pro	Ser	Val	Glu	Leu	Pro	Glu	Lys	Val		
		115					120					125					
agg	att	gct	gtc	gat	act	gta	gtg	aat	gcc	gtt	ggg	gct	gag	cgg	aaa		432
Arg	Ile	Ala	Val	Asp	Thr	Val	Val	Asn	Ala	Val	Gly	Ala	Glu	Arg	Lys		
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Glu	Gln	Val	Ala	Ala	Trp	Thr	Ala	Glu	Lys	Lys	Leu	Ile	Ser	Glu	His		
145					150					155					160		
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Ala	Leu	Thr	Leu	Gln	Gln	Ile	Lys	Ser	Gly	Ile	Val	Ile	Pro	Pro	Ser		
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Gly	Trp	Lys	Cys	Ser	Lys	Cys	Asp	Lys	Thr	Glu	Asn	Leu	Trp	Leu	Asn		
		180						185					190				
ctt	acc	gat	gga	atg	att	ctc	tgt	gga	aga	aaa	aac	tgg	gat	gga	act		624
Leu	Thr	Asp	Gly	Met	Ile	Leu	Cys	Gly	Arg	Lys	Asn	Trp	Asp	Gly	Thr		
		195					200					205					
ggg	gga	aac	aac	cat	gct	gtt	gag	cac	tac	aaa	gag	aca	gcc	tac	cct		672
Gly	Gly	Asn	Asn	His	Ala	Val	Glu	His	Tyr	Lys	Glu	Thr	Ala	Tyr	Pro		
	210					215					220						
ctt	gct	gta	aag	ctt	gga	act	atc	act	gct	gac	tta	gaa	gca	gca	gat		720
Leu	Ala	Val	Lys	Leu	Gly	Thr	Ile	Thr	Ala	Asp	Leu	Glu	Ala	Ala	Asp		
225					230					235					240		
gtt	tat	tcc	tat	ccg	gaa	gat	gac	agt	gtt	ttg	gac	ccg	ctc	ctg	gct		768
Val	Tyr	Ser	Tyr		Pro	Glu	Asp	Asp	Ser	Val	Leu	Asp	Pro	Leu	Leu	Ala	
				245					250					255			
gag	cat	ctg	gcc	cat	ttt	gga	att	gac	ttc	tcg	tcg	atg	cag	aag	act		816
Glu	His	Leu	Ala	His	Phe	Gly	Ile	Asp	Phe	Ser	Ser	Met	Gln	Lys	Thr		
		260						265					270				
gaa	atg	aca	act	gct	gaa	aga	gaa	ctt	gat	caa	aat	aca	aat	ttt	gat		864
Glu	Met	Thr	Thr	Ala	Glu	Arg	Glu	Leu	Asp	Gln	Asn	Thr	Asn	Phe	Asp		
		275					280					285					
tgg	aac	cgt	ata	caa	gag	agt	gga	aaa	gaa	ttg	gtg	cca	gtt	ttt	gga		912
Trp	Asn	Arg	Ile	Gln	Glu	Ser	Gly	Lys	Glu	Leu	Val	Pro	Val	Phe	Gly		
	290					295					300						
cct	gga	tat	acc	gga	ctt	gtc	aat	ctt	ggg	aac	agt	tgc	tac	ttg	gca		960
Pro	Gly	Tyr	Thr	Gly	Leu	Val	Asn	Leu	Gly	Asn	Ser	Cys	Tyr	Leu	Ala		
305					310					315					320		
gct	acg	atg	cag	att	gtt	ttc	tct	acc	cat	tca	ttt	att	tca	aga	tac		1008
Ala	Thr	Met	Gln	Ile	Val	Phe	Ser	Thr	His	Ser	Phe	Ile	Ser	Arg	Tyr		
			325						330					335			
ttt	tca	cat	cag	agc	tta	aag	atg	gct	ttt	gag	atg	gct	cct	gct	gat		1056

Phe	Ser	His	Gln	Ser	Leu	Lys	Met	Ala	Phe	Glu	Met	Ala	Pro	Ala	Asp	
			340					345					350			
cca	act	ttg	gac	ctc	aat	atg	caa	tta	aca	aag	ctt	gga	cac	ggc	tta	1104
Pro	Thr	Leu	Asp	Leu	Asn	Met	Gln	Leu	Thr	Lys	Leu	Gly	His	Gly	Leu	
			355				360					365				
cta	tct	ggg	aag	tac	tca	atg	cct	gca	act	cag	aag	gat	gct	aca	act	1152
Leu	Ser	Gly	Lys	Tyr	Ser	Met	Pro	Ala	Thr	Gln	Lys	Asp	Ala	Thr	Thr	
			370				375					380				
gga	gat	cct	aga	caa	gaa	gga	ata	cct	cct	cgc	atg	ttc	aaa	aac	gta	1200
Gly	Asp	Pro	Arg	Gln	Glu	Gly	Ile	Pro	Pro	Arg	Met	Phe	Lys	Asn	Val	
385					390					395					400	
att	gcc	gcg	agc	cac	gca	gaa	ttc	tct	tct	atg	aga	cag	cag	gat	gct	1248
Ile	Ala	Ala	Ser	His	Ala	Glu	Phe	Ser	Ser	Met	Arg	Gln	Gln	Asp	Ala	
				405					410					415		
ctc	gac	ttt	ttc	ctc	cat	ctg	gta	ggc	aag	gtt	gag	cgt	gct	agc	aac	1296
Leu	Asp	Phe	Phe	Leu	His	Leu	Val	Gly	Lys	Val	Glu	Arg	Ala	Ser	Asn	
			420					425					430			
acg	aca	cca	gat	tta	gac	ccc	tcg	agg	agc	ttc	aag	ttt	gga	ata	gaa	1344
Thr	Thr	Pro	Asp	Leu	Asp	Pro	Ser	Arg	Ser	Phe	Lys	Phe	Gly	Ile	Glu	
			435				440					445				
gag	aag	atc	ctt	tgt	ccg	tct	gga	aag	gtt	gga	tat	aat	aag	agg	gaa	1392
Glu	Lys	Ile	Leu	Cys	Pro	Ser	Gly	Lys	Val	Gly	Tyr	Asn	Lys	Arg	Glu	
	450					455				460						
gac	tgt	att	ctt	tct	ttg	aac	att	ccg	cta	cat	gag	gca	act	aat	aaa	1440
Asp	Cys	Ile	Leu	Ser	Leu	Asn	Ile	Pro	Leu	His	Glu	Ala	Thr	Asn	Lys	
465					470					475					480	
gat	gaa	tta	gaa	gcc	ttt	cac	aag	caa	aaa	gca	gga	aaa	gga	ttg	gaa	1488
Asp	Glu	Leu	Glu	Ala	Phe	His	Lys	Gln	Lys	Ala	Gly	Lys	Gly	Leu	Glu	
				485				490						495		
gag	aat	gat	atg	agg	tca	agt	gat	gaa	ata	gta	cgc	cca	cga	gtt	cct	1536
Glu	Asn	Asp	Met	Arg	Ser	Ser	Asp	Glu	Ile	Val	Arg	Pro	Arg	Val	Pro	
			500					505					510			
tta	gaa	gcc	tgt	cta	gca	aat	ttt	gca	tca	tca	gag	ccg	att	gaa	gac	1584
Leu	Glu	Ala	Cys	Leu	Ala	Asn	Phe	Ala	Ser	Ser	Glu	Pro	Ile	Glu	Asp	
		515					520					525				
tac	tat	agc	tct	gct	ttg	aag	gga	atg	aca	aca	gct	atc	aag	aca	act	1632
Tyr	Tyr	Ser	Ser	Ala	Leu	Lys	Gly	Met	Thr	Thr	Ala	Ile	Lys	Thr	Thr	
		530				535					540					
ggt	ttg	aca	tct	ttc	cca	gat	tat	ttg	gtc	ttg	cac	atg	cgg	aaa	ttt	1680
Gly	Leu	Thr	Ser	Phe	Pro	Asp	Tyr	Leu	Val	Leu	His	Met	Arg	Lys	Phe	
545					550					555					560	
gtt	atg	gag	gaa	ggc	tgg	gtg	cca	aag	aaa	ctt	gat	gta	tac	att	gat	1728
Val	Met	Glu	Glu	Gly	Trp	Val	Pro	Lys	Lys	Leu	Asp	Val	Tyr	Ile	Asp	
				565				570						575		
gtt	ccg	gat	gtt	att	gat	atc	agc	cac	atg	cgt	agc	aaa	gga	ctc	caa	1776

Val	Pro	Asp	Val	Ile	Asp	Ile	Ser	His	Met	Arg	Ser	Lys	Gly	Leu	Gln	
			580					585					590			
cct	ggg	gaa	gaa	ctg	ttg	cca	gat	ggc	gtt	cca	gaa	gaa	gtg	atg	gaa	1824
Pro	Gly	Glu	Glu	Leu	Leu	Pro	Asp	Gly	Val	Pro	Glu	Glu	Val	Met	Glu	
		595					600					605				
tca	gcg	cag	ccc	gtg	gca	aat	gag	gag	ata	gtt	gca	cag	cta	gtc	tca	1872
Ser	Ala	Gln	Pro	Val	Ala	Asn	Glu	Glu	Ile	Val	Ala	Gln	Leu	Val	Ser	
	610					615					620					
atg	gga	ttt	agc	cag	ctt	cac	tgc	cag	aaa	gct	gcc	ata	aat	act	tcc	1920
Met	Gly	Phe	Ser	Gln	Leu	His	Cys	Gln	Lys	Ala	Ala	Ile	Asn	Thr	Ser	
	625				630				635					640		
aat	gct	ggg	gtt	gaa	gag	gca	atg	aac	tgg	tta	ctt	tct	cac	atg	gat	1968
Asn	Ala	Gly	Val	Glu	Glu	Ala	Met	Asn	Trp	Leu	Leu	Ser	His	Met	Asp	
			645					650						655		
gat	cca	gac	atc	gat	gca	cca	atc	tcc	cac	cag	aca	tct	gac	att	gat	2016
Asp	Pro	Asp	Ile	Asp	Ala	Pro	Ile	Ser	His	Gln	Thr	Ser	Asp	Ile	Asp	
			660					665					670			
caa	tca	agc	gtt	gat	acc	tta	ctc	tcc	ttt	ggg	ttt	gct	gaa	gat	gtt	2064
Gln	Ser	Ser	Val	Asp	Thr	Leu	Leu	Ser	Phe	Gly	Phe	Ala	Glu	Asp	Val	
		675					680					685				
gct	cgg	aag	gca	cta	aaa	gcc	tcg	gga	gga	gac	att	gag	aaa	gca	aca	2112
Ala	Arg	Lys	Ala	Leu	Lys	Ala	Ser	Gly	Gly	Asp	Ile	Glu	Lys	Ala	Thr	
	690					695				700						
gac	tgg	gta	ttc	aac	aac	cct	aat	gca	tct	gtt	tca	gac	atg	gat	gta	2160
Asp	Trp	Val	Phe	Asn	Asn	Pro	Asn	Ala	Ser	Val	Ser	Asp	Met	Asp	Val	
	705				710					715					720	
tcc	tct	agc	aat	tca	gcg	cag	act	ccg	gct	caa	agt	gga	tta	cca	gat	2208
Ser	Ser	Ser	Asn	Ser	Ala	Gln	Thr	Pro	Ala	Gln	Ser	Gly	Leu	Pro	Asp	
			725						730					735		
gga	gga	ggg	aaa	tac	aag	ctg	ttt	gga	ata	gta	agt	cac	atg	gga	aca	2256
Gly	Gly	Gly	Lys	Tyr	Lys	Leu	Phe	Gly	Ile	Val	Ser	His	Met	Gly	Thr	
			740					745					750			
tca	gtg	cac	tgt	ggg	cat	tac	gtg	gct	cac	ata	ttg	aaa	gaa	ggc	cgc	2304
Ser	Val	His	Cys	Gly	His	Tyr	Val	Ala	His	Ile	Leu	Lys	Glu	Gly	Arg	
		755					760					765				
tgg	gta	att	ttc	aat	gac	gac	aaa	gtt	ggg	atc	tcg	act	gat	cct	cct	2352
Trp	Val	Ile	Phe	Asn	Asp	Asp	Lys	Val	Gly	Ile	Ser	Thr	Asp	Pro	Pro	
	770					775					780					
aaa	gac	atg	ggg	tat	gtc	tac	ttc	ttt	cag	cgg	ctt	gat	tga			2394
Lys	Asp	Met	Gly	Tyr	Val	Tyr	Phe	Phe	Gln	Arg	Leu	Asp				
	785				790				795							

&lt;210&gt; 30

&lt;211&gt; 797

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 30

Met Glu Leu Leu Arg Ser Asn Leu Ser Arg Val Gln Ile Pro Glu Pro  
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Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro  
 20 25 30

Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe  
 35 40 45

Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val  
 50 55 60

Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro  
 65 70 75 80

Leu Lys Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Gly Phe Asp  
 85 90 95

Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro  
 100 105 110

Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val  
 115 120 125

Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys  
 130 135 140

Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His  
 145 150 155 160

Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser  
 165 170 175

Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn  
 180 185 190

Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr  
 195 200 205

Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro  
 210 215 220

Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp  
 225 230 235 240

Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala  
 245 250 255

Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr  
 260 265 270

Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp  
 275 280 285

Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly  
 290 295 300

Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala  
 305 310 315 320

Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr  
 325 330 335

Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp  
 340 345 350

Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu  
 355 360 365

Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr  
 370 375 380

Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val  
 385 390 395 400

Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala  
 405 410 415

Leu Asp Phe Phe Leu His Leu Val Gly Lys Val Glu Arg Ala Ser Asn  
 420 425 430

Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu  
 435 440 445



Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu  
 450 455 460

Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys  
 465 470 475 480

Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Leu Glu  
 485 490 495

Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro  
 500 505 510

Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp  
 515 520 525

Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr  
 530 535 540

Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe  
 545 550 555 560

Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp  
 565 570 575

Val Pro Asp Val Ile Asp Ile Ser His Met Arg Ser Lys Gly Leu Gln  
 580 585 590

Pro Gly Glu Glu Leu Leu Pro Asp Gly Val Pro Glu Glu Val Met Glu  
 595 600 605

Ser Ala Gln Pro Val Ala Asn Glu Glu Ile Val Ala Gln Leu Val Ser  
 610 615 620

Met Gly Phe Ser Gln Leu His Cys Gln Lys Ala Ala Ile Asn Thr Ser  
 625 630 635 640

Asn Ala Gly Val Glu Glu Ala Met Asn Trp Leu Leu Ser His Met Asp  
 645 650 655

Asp Pro Asp Ile Asp Ala Pro Ile Ser His Gln Thr Ser Asp Ile Asp  
 660 665 670

Gln Ser Ser Val Asp Thr Leu Leu Ser Phe Gly Phe Ala Glu Asp Val  
 675 680 685

Ala Arg Lys Ala Leu Lys Ala Ser Gly Gly Asp Ile Glu Lys Ala Thr  
 690 695 700

Asp Trp Val Phe Asn Asn Pro Asn Ala Ser Val Ser Asp Met Asp Val  
 705 710 715 720

Ser Ser Ser Asn Ser Ala Gln Thr Pro Ala Gln Ser Gly Leu Pro Asp  
 725 730 735

Gly Gly Gly Lys Tyr Lys Leu Phe Gly Ile Val Ser His Met Gly Thr  
 740 745 750

Ser Val His Cys Gly His Tyr Val Ala His Ile Leu Lys Glu Gly Arg  
 755 760 765

Trp Val Ile Phe Asn Asp Asp Lys Val Gly Ile Ser Thr Asp Pro Pro  
 770 775 780

Lys Asp Met Gly Tyr Val Tyr Phe Phe Gln Arg Leu Asp  
 785 790 795

<210> 31

<211> 1068

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1068)

<223> 15377

<400> 31

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1				5					10					15		

tct	ata	gct	cca	tca	ccg	aag	aag	aag	cct	ctc	atc	ttc	tta	ggc	tct	96
Ser	Ile	Ala	Pro	Ser	Pro	Lys	Lys	Lys	Pro	Leu	Ile	Phe	Leu	Gly	Ser	
			20					25					30			

cct	cag	gtc	tcc	gtg	agt	gtg	ctt	gaa	gct	ctt	ttc	aat	gca	tct	aat	144
Pro	Gln	Val	Ser	Val	Ser	Val	Leu	Glu	Ala	Leu	Phe	Asn	Ala	Ser	Asn	
		35					40					45				

gct cca aac tct tcc ttc gag gtt gca ggt att gtt aca cag cct cca Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro 50 55 60	192
tca agg aga gat agg ggt aaa aaa gtg ttg cct tca cca gta gcg caa Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln 65 70 75 80	240
tac gct ctt gat aaa ggc tta cct tct gat ctc att ttc tcc cct gag Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu 85 90 95	288
aag gca gga gat gaa gca ttt tta tcg gct tta aga gag ttg caa cct Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro 100 105 110	336
gag ctt tgt att aca gca gct tat ggg aat att ttg cct act aag ttc Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe 115 120 125	384
ctt aag att ccg gta cat ggg aca gtg aac ata cac cca agt ttg ctg Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu 130 135 140	432
ccg ctg tac cgt ggt gca gct cca gtt caa aga gca tta cag gat ggt Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly 145 150 155 160	480
gtc ccg gaa aca gga gta tca tta gca ttt act gtg cgt aag tta gat Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp 165 170 175	528
gca ggg cca gtg att gcc tct aag agg ttc caa gtg gat gat cta ata Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile 180 185 190	576
aag gca cca gaa cta ctc tcg ttc cta ttt tct gaa ggt tct aat ctt Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu 195 200 205	624
ctt atc cgt gaa ctt ccc tcg ata ttt gat ggg tcc gca aaa tca aaa Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys 210 215 220	672
gca gct ccc caa gat gat tct aaa gct acc tta gct cca aag ata gct Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala 225 230 235 240	720
cca gat gag gct tgg ctc tct ttt gac cag gaa gct ttt gtt cta cat Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His 245 250 255	768
aac aag gtt cgt gca ttt gca gga tgg ccg gga aca cga gca aaa gtt Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val 260 265 270	816
gta gtc ctt gat gag aaa agc ggt cag caa aat gtg cta gag ctt aaa Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys 275 280 285	864

att atg tcc act cga gta tgc aaa gat ctg gaa att cag gat agt gaa 912  
 Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu  
 290 295 300  
  
 caa gat tat gta act ttc aag aaa ggt tca cta ata ttt ccc tgc aga 960  
 Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu Ile Phe Pro Cys Arg  
 305 310 315 320  
  
 gga ggt aca gct tta gag gta ctg gaa gtc cag ctt cct ggt aag aaa 1008  
 Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys  
 325 330 335  
  
 gcc atc aac gca gct gct ttt tgg aat ggc ttg aga ggt caa aag ctg 1056  
 Ala Ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu  
 340 345 350  
  
 aag aag cta tga 1068  
 Lys Lys Leu  
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<211> 355

<212> PRT

<213> Arabidopsis thaliana

<400> 32

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 Pro Gln Val Ser Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn  
 35 40 45  
  
 Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro  
 50 55 60  
  
 Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln  
 65 70 75 80  
  
 Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu  
 85 90 95  
  
 Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro  
 100 105 110

Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe  
 115 120 125

Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu  
 130 135 140

Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly  
 145 150 155 160

Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp  
 165 170 175

Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile  
 180 185 190

Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu  
 195 200 205

Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys  
 210 215 220

Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala  
 225 230 235 240

Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His  
 245 250 255

Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val  
 260 265 270

Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys  
 275 280 285

Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu  
 290 295 300

Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu Ile Phe Pro Cys Arg  
 305 310 315 320

Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys  
 325 330 335

Ala Ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu  
 340 345 350

Lys Lys Leu  
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<210> 33

<211> 2220

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2220)

<223> 16219

<400> 33

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aat cct ctc tcc tac tta gtc tcc att gat ggt ttc aac ttc ctc atc	96
Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile	
20 25 30	

gac tgt ggt tgg aac gat ctc ttc gac aca tcg ctc ctc gaa cct ctc	144
Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu	
35 40 45	

ccc agg gtt gct tct act ata gat gca gtt ttg ctt tct cat cca gat	192
Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp	
50 55 60	

aca ctt cac att ggt gct ctt cct tat gct atg aag cag ctt gga ctc	240
Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu	
65 70 75 80	

tcc gct cct gtt tat gct act gag cct gtt cat aga tta ggt ctc ctt	288
Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu	
85 90 95	

aca atg tat gat cag ttt ttg tcc agg aag caa gta tcc gac ttt gat	336
Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp	
100 105 110	

ctg ttt aca ctg gat gac ata gat tct gct ttc cag aat gtg atc aga	384
Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg	
115 120 125	

ttg act tac tct caa aat tac cat ctt tct gga aag gga gag ggt att	432
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Leu	Thr	Tyr	Ser	Gln	Asn	Tyr	His	Leu	Ser	Gly	Lys	Gly	Glu	Gly	Ile	
130						135					140					
gta	att	gct	cct	cat	gtt	gct	gga	cac	atg	ctg	gga	ggt	agc	atc	tgg	480
Val	Ile	Ala	Pro	His	Val	Ala	Gly	His	Met	Leu	Gly	Gly	Ser	Ile	Trp	
145					150					155					160	
agg	ata	aca	aag	gat	ggg	gag	gat	gtt	ata	tat	gct	gtt	gac	tac	aat	528
Arg	Ile	Thr	Lys	Asp	Gly	Glu	Asp	Val	Ile	Tyr	Ala	Val	Asp	Tyr	Asn	
				165					170					175		
cat	cgg	aaa	gaa	agg	cat	ttg	aat	gga	act	gtt	tta	cag	tct	ttt	gtt	576
His	Arg	Lys	Glu	Arg	His	Leu	Asn	Gly	Thr	Val	Leu	Gln	Ser	Phe	Val	
			180					185					190			
cgg	cct	gct	gtt	ctg	ata	acc	gat	gca	tat	cat	gct	ctt	tat	acc	aat	624
Arg	Pro	Ala	Val	Leu	Ile	Thr	Asp	Ala	Tyr	His	Ala	Leu	Tyr	Thr	Asn	
		195					200					205				
caa	acc	gca	aga	cag	caa	agg	gac	aaa	gaa	ttt	cta	gat	acc	att	tca	672
Gln	Thr	Ala	Arg	Gln	Gln	Arg	Asp	Lys	Glu	Phe	Leu	Asp	Thr	Ile	Ser	
	210					215					220					
aaa	cat	ctt	gaa	gtt	gga	gga	aat	gtt	cta	ttg	cca	gta	gac	act	gcg	720
Lys	His	Leu	Glu	Val	Gly	Gly	Asn	Val	Leu	Leu	Pro	Val	Asp	Thr	Ala	
225					230				235						240	
ggg	cgt	gtc	ctg	gaa	ctt	ctc	ttg	ata	ctt	gaa	cag	cat	tgg	tca	caa	768
Gly	Arg	Val	Leu	Glu	Leu	Leu	Leu	Ile	Leu	Glu	Gln	His	Trp	Ser	Gln	
				245					250					255		
aga	ggg	ttc	agc	ttt	ccc	att	tat	ttt	ctc	acg	tac	gtg	tca	tct	agc	816
Arg	Gly	Phe	Ser	Phe	Pro	Ile	Tyr	Phe	Leu	Thr	Tyr	Val	Ser	Ser	Ser	
			260					265					270			
aca	att	gac	tat	gtt	aag	agt	ttc	ctc	gag	tgg	atg	agt	gac	tcc	att	864
Thr	Ile	Asp	Tyr	Val	Lys	Ser	Phe	Leu	Glu	Trp	Met	Ser	Asp	Ser	Ile	
		275					280					285				
tca	aag	tcc	ttt	gag	act	tca	cgt	gat	aat	gcc	ttt	cta	ttg	agg	cat	912
Ser	Lys	Ser	Phe	Glu	Thr	Ser	Arg	Asp	Asn	Ala	Phe	Leu	Leu	Arg	His	
	290					295					300					
gtc	act	ctg	ttg	ata	aac	aag	act	gat	ctg	gat	aat	gct	cca	cct	ggt	960
Val	Thr	Leu	Leu	Ile	Asn	Lys	Thr	Asp	Leu	Asp	Asn	Ala	Pro	Pro	Gly	
305					310					315					320	
cca	aag	gtt	gtt	ctt	gct	tcc	atg	gct	agt	ctc	gaa	gcc	ggt	ttt	gct	1008
Pro	Lys	Val	Val	Leu	Ala	Ser	Met	Ala	Ser	Leu	Glu	Ala	Gly	Phe	Ala	
				325					330					335		
cga	gag	ata	ttc	gtg	gag	tgg	gca	aat	gat	ccc	aga	aat	tta	gtc	ctc	1056
Arg	Glu	Ile	Phe	Val	Glu	Trp	Ala	Asn	Asp	Pro	Arg	Asn	Leu	Val	Leu	
			340					345					350			
ttt	act	gaa	aca	ggc	cag	ttt	ggc	act	tta	gct	cgt	atg	ctt	cag	tca	1104
Phe	Thr	Glu	Thr	Gly	Gln	Phe	Gly	Thr	Leu	Ala	Arg	Met	Leu	Gln	Ser	
		355					360					365				
gcc	cca	cct	cca	aaa	ttt	gtt	aaa	gtc	acc	atg	tct	aag	agg	gtt	cct	1152

Ala	Pro	Pro	Pro	Lys	Phe	Val	Lys	Val	Thr	Met	Ser	Lys	Arg	Val	Pro	
370						375					380					
ttg	gct	ggg	gaa	gag	tta	att	gca	tat	gag	gaa	gag	caa	aac	aga	ctg	1200
Leu	Ala	Gly	Glu	Glu	Leu	Ile	Ala	Tyr	Glu	Glu	Glu	Gln	Asn	Arg	Leu	
385					390				395						400	
aaa	agg	gaa	gaa	gct	ttg	cga	gct	agc	ctc	gtt	aaa	gag	gag	gaa	aca	1248
Lys	Arg	Glu	Glu	Ala	Leu	Arg	Ala	Ser	Leu	Val	Lys	Glu	Glu	Glu	Thr	
				405					410					415		
aaa	gct	tcc	cat	gga	tcc	gat	gat	aat	tca	agt	gaa	cct	atg	atc	ata	1296
Lys	Ala	Ser	His	Gly	Ser	Asp	Asp	Asn	Ser	Ser	Glu	Pro	Met	Ile	Ile	
			420					425					430			
gat	acc	aag	act	act	cac	gat	gtt	gtt	ggt	tct	cac	ggg	cct	gca	tat	1344
Asp	Thr	Lys	Thr	Thr	His	Asp	Val	Val	Gly	Ser	His	Gly	Pro	Ala	Tyr	
		435					440					445				
aaa	gat	ata	ttg	att	gat	gga	ttt	gtt	ccc	cca	tcg	agc	agc	gta	gct	1392
Lys	Asp	Ile	Leu	Ile	Asp	Gly	Phe	Val	Pro	Pro	Ser	Ser	Ser	Val	Ala	
	450					455					460					
cca	atg	ttc	cca	tat	tat	gat	aac	aca	tct	gaa	tgg	gac	gac	ttt	ggg	1440
Pro	Met	Phe	Pro	Tyr	Tyr	Asp	Asn	Thr	Ser	Glu	Trp	Asp	Asp	Phe	Gly	
465					470				475						480	
gag	att	att	aat	cca	gat	gac	tat	gtg	atc	aag	gat	gaa	gac	atg	gac	1488
Glu	Ile	Ile	Asn	Pro	Asp	Asp	Tyr	Val	Ile	Lys	Asp	Glu	Asp	Met	Asp	
			485					490						495		
cga	gga	gca	atg	cat	aac	gga	ggt	gat	gtg	gac	gga	agg	ctt	gat	gag	1536
Arg	Gly	Ala	Met	His	Asn	Gly	Gly	Asp	Val	Asp	Gly	Arg	Leu	Asp	Glu	
			500					505					510			
gca	act	gct	agt	ctc	atg	ctt	gat	aca	aga	cct	tcg	aaa	gtc	atg	tcc	1584
Ala	Thr	Ala	Ser	Leu	Met	Leu	Asp	Thr	Arg	Pro	Ser	Lys	Val	Met	Ser	
		515					520					525				
aat	gag	ctc	att	gtg	act	gtt	agt	tgt	tca	ctt	gtt	aaa	atg	gac	tat	1632
Asn	Glu	Leu	Ile	Val	Thr	Val	Ser	Cys	Ser	Leu	Val	Lys	Met	Asp	Tyr	
	530					535					540					
gaa	ggt	cgg	tca	gat	ggc	cgc	tca	atc	aag	tca	atg	att	gcg	cat	gtt	1680
Glu	Gly	Arg	Ser	Asp	Gly	Arg	Ser	Ile	Lys	Ser	Met	Ile	Ala	His	Val	
545					550				555						560	
tct	cct	cta	aaa	ctt	gtt	ttg	gtg	cac	gcg	ata	gct	gag	gct	aca	gag	1728
Ser	Pro	Leu	Lys	Leu	Val	Leu	Val	His	Ala	Ile	Ala	Glu	Ala	Thr	Glu	
				565				570						575		
cat	ttg	aag	caa	cac	tgc	ttg	aac	aac	atc	tgt	cca	cac	gtg	tat	gct	1776
His	Leu	Lys	Gln	His	Cys	Leu	Asn	Asn	Ile	Cys	Pro	His	Val	Tyr	Ala	
			580					585					590			
cct	caa	ata	gag	gaa	acg	gtc	gat	gtg	act	tct	gat	tta	tgt	gct	tac	1824
Pro	Gln	Ile	Glu	Glu	Thr	Val	Asp	Val	Thr	Ser	Asp	Leu	Cys	Ala	Tyr	
		595				600						605				
aag	gtc	caa	ctt	tct	gaa	aag	ctg	atg	agc	aat	gtg	atc	ttc	aag	aag	1872



Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys	
610 615 620	
ctg gga gat tca gaa gta gct tgg gtg gat tcc gaa gta ggg aag aca	1920
Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr	
625 630 635 640	
gag agg gac atg agg tct cta cta ccg atg cca ggt gct gct tcg cca	1968
Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro	
645 650 655	
cac aaa cct gtt cta gta ggt gat ctg aaa atc gca gac ttc aag cag	2016
His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln	
660 665 670	
ttt ctg tcg agc aag ggt gtt cag gta gaa ttt gca ggt gga gga gct	2064
Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Gly Ala	
675 680 685	
tta cgt tgt ggt gaa tat gtc act cta cga aag gtt gga ccg acg ggt	2112
Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly	
690 695 700	
caa aag gga gga gca tcg ggt cca cag caa att ctg ata gaa gga ccg	2160
Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro	
705 710 715 720	
ttg tgt gaa gac tat tac aaa atc agg gat tat ctc tat tct cag ttc	2208
Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe	
725 730 735	
tac ctc ctc tga	2220
Tyr Leu Leu	

&lt;210&gt; 34

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 34

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Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile
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Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu
35 40 45

Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp  
 50 55 60

Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu  
 65 70 75 80

Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu  
 85 90 95

Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp  
 100 105 110

Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg  
 115 120 125

Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile  
 130 135 140

Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp  
 145 150 155 160

Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn  
 165 170 175

His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val  
 180 185 190

Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn  
 195 200 205

Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser  
 210 215 220

Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala  
 225 230 235 240

Gly Arg Val Leu Glu Leu Leu Leu Ile Leu Glu Gln His Trp Ser Gln  
 245 250 255

Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser  
 260 265 270

Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile  
 275 280 285

Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His  
 290 295 300

Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly  
 305 310 315 320

Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala  
 325 330 335

Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu  
 340 345 350

Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser  
 355 360 365

Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro  
 370 375 380

Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Glu Gln Asn Arg Leu  
 385 390 395 400

Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Glu Thr  
 405 410 415

Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile  
 420 425 430

Asp Thr Lys Thr Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr  
 435 440 445

Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Ser Val Ala  
 450 455 460

Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly  
 465 470 475 480

Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp  
 485 490 495

Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu  
 500 505 510

Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser  
 515 520 525

Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr  
 530 535 540

Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val  
 545 550 555 560

Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu  
 565 570 575

His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala  
 580 585 590

Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr  
 595 600 605

Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys  
 610 615 620

Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr  
 625 630 635 640

Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro  
 645 650 655

His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln  
 660 665 670

Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Gly Ala  
 675 680 685

Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly  
 690 695 700

Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro  
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Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe  
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Tyr Leu Leu

<210> 35

<211> 1116

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1116)

&lt;223&gt;

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atc cca ttc aaa cgg acc ttg ttt tct tca atc cat tat ccg gcc aaa      96
Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys
          20          25          30

acc ctt ctt cta cga cca cta aaa ccg tcg gaa gtt cct tcc ttt cgc      144
Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg
          35          40          45

cgg acg atc atc act ttc cag aaa att tca acc ggg att gtt cct cca      192
Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro
          50          55          60

cca tcg gct tca tca tct ccg tcg agc tat gga gac ctt caa cca atc      240
Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile
65          70          75          80

gaa gag ctt cca ccg aag cta caa gag atc gtc aag ctt ttc caa tcg      288
Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser
          85          90          95

gta caa gag cca aag gct aaa tac gag cag ctt atg ttc tac ggg aag      336
Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys
          100          105          110

aat ctg aca cct ctc gat tct caa ttc aag acg agg gag aat aaa gta      384
Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val
          115          120          125

gaa gga tgt gtt tct cag gtt tgg gtt agg gct ttc ttt gat gag gaa      432
Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu
          130          135          140

cgt aat gtt gtg tat gaa gct gat tct gat tcg gtt ctc act aaa ggg      480
Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
          145          150          155          160

tta gct gct cta tta gtc aag ggt tta tct gga aga cct gtc cct gag      528
Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
          165          170          175

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att ttg agg ata aca cct gat ttc gct gtt ctt ctc ggg ttg cag cag 576  
 Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln  
 180 185 190

agt ctg tct cct tct aga aac aat gga tta ctt aat atg ctt aag ctg 624  
 Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu  
 195 200 205

atg cag aaa aag gct ctt cat ttg gaa gtc aaa ggt gag gaa gat tca 672  
 Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser  
 210 215 220

agt tct gga gag agt tca gaa tcc agc ttt gtg tct att cct gag act 720  
 Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr  
 225 230 235 240

aag gac gaa gct aat gtt ccg gag gtg gat ttg gag tct aaa cct gat 768  
 Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp  
 245 250 255

cta gtt gag gat ttg gga aca gaa aag att gat gat tct gag agt ggg 816  
 Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly  
 260 265 270

tca aat gtt gtt gct tta ggg agt aga ggg atg agg ata aga gag aaa 864  
 Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys  
 275 280 285

ttg gag aag gag cta gat cct gtt gag tta gaa gtt gaa gat gtt tct 912  
 Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser  
 290 295 300

tac cag cac gca gga cat gcc gct gtt aga ggt agt gct ggt gat gat 960  
 Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp  
 305 310 315 320

ggg gaa aca cat ttc aac ttg cga atc gtt tcg gat gct ttc caa ggt 1008  
 Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly  
 325 330 335

aaa agc ttg gtc aag aga cat agg ctg ata tat gac ttg ttg caa gat 1056  
 Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp  
 340 345 350

gag ttg aag agc ggg tta cat gct ctc tct att gtg gca aag act cct 1104  
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 355 360 365

gct gag gtt tga 1116  
 Ala Glu Val  
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&lt;210&gt; 36

&lt;211&gt; 371

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 36

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Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys  
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Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg  
 35 40 45

Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro  
 50 55 60

Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile  
 65 70 75 80

Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser  
 85 90 95

Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys  
 100 105 110

Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val  
 115 120 125

Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu  
 130 135 140

Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly  
 145 150 155 160

Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu  
 165 170 175

Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln  
 180 185 190

Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu  
 195 200 205

Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser  
 210 215 220

Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr  
 225 230 235 240

Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp  
 245 250 255

Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly  
 260 265 270

Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys  
 275 280 285

Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser  
 290 295 300

Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp  
 305 310 315 320

Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly  
 325 330 335

Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp  
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Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro  
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<210> 37

<211> 1059

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1059)

<223> 20933



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gaa ggc cac acc gat cgt gtt tgg agc gta gct tgg aac ccc gtt tct 96  
 Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser  
 20 25 30

tct cac gcc gac ggt gtt tca ccg att ctt gct tct tgc agt ggc gat 144  
 Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp  
 35 40 45

aac act gtt cga atc tgg gaa caa agc tct ctc tct cgc tcc tgg act 192  
 Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr  
 50 55 60

tgc aag aca gtt ttg gaa gag acg cat aca aga act gtg agg tcg tgc 240  
 Cys Lys Thr Val Leu Glu Glu Thr His Thr Arg Thr Val Arg Ser Cys  
 65 70 75 80

gct tgg tca ccc tca gga cag tta ttg gcc act gca agt ttt gat ggt 288  
 Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly  
 85 90 95

acc act ggc att tgg aag aat tac ggt tct gag ttt gag tgt att tcc 336  
 Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser  
 100 105 110

act ttg gag gga cat gaa aac gaa gtc aaa agt gta tca tgg aat gca 384  
 Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala  
 115 120 125

tct ggt tca tgc ctt gca aca tgt agt aga gat aag tct gtt tgg att 432  
 Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile  
 130 135 140

tgg gaa gtg ctt gaa ggg aat gaa tat gac tgt gct gcg gta tta act 480  
 Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr  
 145 150 155 160

ggg cat aca caa gat gtg aag atg gtt cag tgg cat ccc acc atg gat 528  
 Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp  
 165 170 175

ggt tta ttt tct tgc agt tat gat aac acc atc aag gtt tgg tgg tct 576  
 Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser  
 180 185 190

gaa gat gat gat ggt gag tat caa tgt gtc caa acc tta ggt gaa tct 624  
 Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser  
 195 200 205

aac aac ggt cac tct tca acg gta tgg tcc atc tca ttt aac gct gca 672  
 Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala  
 210 215 220

ggg gac aag atg gtc act tgt agt gat gat cta acc ttg aag ata tgg 720

Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp  
 225 230 235 240  
 ggg aca gat att gcc aag atg cag tct ggt gaa gaa tat gca cct tgg 768  
 Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp  
 245 250 255  
 att cat ctt tgt act ctc tct ggc tat cat gac cgt acc ata tac tca 816  
 Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser  
 260 265 270  
 gct cac tgg tca agg gac gac att att gcc agt gga gca ggc gat aat 864  
 Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn  
 275 280 285  
 gct ata cgg ttg ttt gtg gac agc aaa cat gac tct gtt gat gga cct 912  
 Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro  
 290 295 300  
 tca tat aat ctt ttg ctg aag aag aat aaa gca cat gaa aat gat gta 960  
 Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val  
 305 310 315 320  
 aac tct gtc caa tgg tca ccc ggt gag ggg aac cgg ttg ctt gcg tcg 1008  
 Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser  
 325 330 335  
 gct agt gat gat ggg atg gtc aag att tgg cag ctt gca act aaa ccg 1056  
 Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro  
 340 345 350  
 tga 1059

&lt;210&gt; 38

&lt;211&gt; 352

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 38

Met Asp Leu Met Glu Lys Asn Leu Glu Leu Val Glu Ile Gln Lys Leu  
 1 5 10 15  
 Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser  
 20 25 30  
 Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp  
 35 40 45  
 Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr  
 50 55 60

Cys Lys Thr Val Leu Glu Thr His Thr Arg Thr Val Arg Ser Cys  
 65 70 75 80

Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly  
 85 90 95

Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser  
 100 105 110

Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala  
 115 120 125

Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile  
 130 135 140

Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr  
 145 150 155 160

Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp  
 165 170 175

Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser  
 180 185 190

Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser  
 195 200 205

Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala  
 210 215 220

Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp  
 225 230 235 240

Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp  
 245 250 255

Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser  
 260 265 270

Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn  
 275 280 285

Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro  
 290 295 300

Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val  
305 310 315 320

Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser  
325 330 335

Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro  
340 345 350

<210> 39

<211> 942

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(924)

<223>

<400> 39  
atg cta agc ttg aga tat tca tta cct tat ctt ctt ctt caa aca agg 48  
Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg  
1 5 10 15  
gaa tca tca act aag ctc ttc acc aaa aag cct aac aat gtt gtg gtt 96  
Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val  
20 25 30  
tgt gcg gcg aga ggt cca aga cct cgg tct cct cgt gta tgg aaa aca 144  
Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr  
35 40 45  
agg aag agg att gga act atc tct aaa gct gcc aaa atg att gct tgt 192  
Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys  
50 55 60  
ata aaa gga ttg tcg aat gtt aaa gaa gaa gtt tat gga gcg ctt gat 240  
Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp  
65 70 75 80  
tcc ttc att gct tgg gaa tta gag ttc cct ctt gtt ata gtt aag aag 288  
Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys  
85 90 95  
gca tta gtt ata ctt gaa gat gaa aaa gaa tgg aag aag att att cag 336  
Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln

100	105	110	
gtg aca aaa tgg atg ctg agt aaa ggc caa gga aga aca atg gga act			384
Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr			
115	120	125	
tac ttc tca tta cta aat gct tta gca gaa gat aat cgc ctt gac gaa			432
Tyr. Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu			
130	135	140	
gct gag gaa ttg tgg aac aaa ttg ttc atg gaa cat tta gaa gga act			480
Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr			
145	150	155	160
cct aga aag ttc ttc aac aaa atg atc tct ata tat tac aag aga gat			528
Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp			
165	170	175	
atg cac caa aag ctc ttc gag gtc ttt gct gac atg gag gag ctt gga			576
Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly			
180	185	190	
gtg aaa ccg aat gtt gcg att gtg tct atg gtt gga aaa gtg ttt gtg			624
Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val			
195	200	205	
aaa cta gag atg aag gat aag tac gag aaa ctg atg aag aaa tat cct			672
Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro			
210	215	220	
cca cca cag tgg gag ttt aga tac atc aaa gga aga cgt gtt aag gtc			720
Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val			
225	230	235	240
aag gca aag cag ctg aat gag cta agc gaa ggt gaa ggt ggt tta agc			768
Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Gly Leu Ser			
245	250	255	
agc gac gaa gat aag att gac aat gag att gag agt gaa gaa gaa gat			816
Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Glu Asp			
260	265	270	
ggt gag gat ctc agt gaa gag gaa gaa gat gaa aaa gaa ctt ttg ggt			864
Gly Glu Asp Leu Ser Glu Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly			
275	280	285	
gga agt caa gga cag att act tct aga gaa ccc agt ctt gat cat ttg			912
Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu			
290	295	300	
gac tct tca tga			924
Asp Ser Ser			
305			

&lt;210&gt; 40

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 40

Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg  
 1 5 10 15

Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val  
 20 25 30

Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr  
 35 40 45

Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys  
 50 55 60

Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp  
 65 70 75 80

Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys  
 85 90 95

Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln  
 100 105 110

Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr  
 115 120 125

Tyr Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu  
 130 135 140

Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr  
 145 150 155 160

Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp  
 165 170 175

Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly  
 180 185 190

Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val  
 195 200 205

Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro  
 210 215 220

Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val  
 225 230 235 240

Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Gly Leu Ser  
 245 250 255

Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Glu Asp  
 260 265 270

Gly Glu Asp Leu Ser Glu Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly  
 275 280 285

Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu  
 290 295 300

Asp Ser Ser  
 305

<210> 41

<211> 2427

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2427)

<223> 21878

<400> 41  
 atg gta aag gaa act cta att cct ccg tca tct acg tca atg acg acc 48  
 Met Val Lys Glu Thr Leu Ile Pro Pro Ser Ser Thr Ser Met Thr Thr  
 1 5 10 15

gga aca tct tct tct tcg tct ctt tca atg acg tta tcc tca aca aac 96  
 Gly Thr Ser Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn  
 20 25 30

gcg tta tcg ttt ttg tcg aaa gga tgg aga gag gta tgg gat tca gca 144  
 Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala

35					40					45										
gat	gcg	gat	ttg	cag	ctg	atg	cga	gac	aga	gct	aac	tct	gtt	aag	aat	192				
Asp	Ala	Asp	Leu	Gln	Leu	Met	Arg	Asp	Arg	Ala	Asn	Ser	Val	Lys	Asn					
50					55					60										
cta	gca	tca	acg	ttc	gat	aga	gag	atc	gag	aat	ttc	ctc	aat	aac	tcg	240				
Leu	Ala	Ser	Thr	Phe	Asp	Arg	Glu	Ile	Glu	Asn	Phe	Leu	Asn	Asn	Ser					
65					70					75					80					
gcg	agg	tct	gcg	ttt	ccc	gtt	ggg	tca	cca	tcg	gcg	tcg	tct	ttc	tca	288				
Ala	Arg	Ser	Ala	Phe	Pro	Val	Gly	Ser	Pro	Ser	Ala	Ser	Ser	Phe	Ser					
85					90					95										
aat	gaa	att	ggg	atc	atg	aag	aag	ctt	cag	ccg	aag	att	tcg	gag	ttt	336				
Asn	Glu	Ile	Gly	Ile	Met	Lys	Lys	Leu	Gln	Pro	Lys	Ile	Ser	Glu	Phe					
100					105					110										
cgt	agg	gtt	tat	tcg	gcg	ccg	gag	att	agt	cgc	aag	gtt	atg	gag	aga	384				
Arg	Arg	Val	Tyr	Ser	Ala	Pro	Glu	Ile	Ser	Arg	Lys	Val	Met	Glu	Arg					
115					120					125										
tgg	gga	cct	gcg	aga	gcg	aag	ctt	gga	atg	gat	cta	tcg	gcg	att	aag	432				
Trp	Gly	Pro	Ala	Arg	Ala	Lys	Leu	Gly	Met	Asp	Leu	Ser	Ala	Ile	Lys					
130					135					140										
aag	gcg	att	gtg	tct	gag	atg	gaa	ttg	gat	gag	cgt	cag	gga	gtt	ttg	480				
Lys	Ala	Ile	Val	Ser	Glu	Met	Glu	Leu	Asp	Glu	Arg	Gln	Gly	Val	Leu					
145					150					155					160					
gag	atg	agt	aga	ttg	agg	aga	cgg	cgt	aat	agt	gat	agg	gtt	agg	ttt	528				
Glu	Met	Ser	Arg	Leu	Arg	Arg	Arg	Arg	Asn	Ser	Asp	Arg	Val	Arg	Phe					
165					170					175										
acg	gag	ttt	ttc	gcg	gag	gct	gag	aga	gat	gga	gaa	gct	tat	ttc	ggg	576				
Thr	Glu	Phe	Phe	Ala	Glu	Ala	Glu	Arg	Asp	Gly	Glu	Ala	Tyr	Phe	Gly					
180					185					190										
gat	tgg	gaa	ccg	att	agg	tct	ttg	aag	agt	aga	ttt	aaa	gag	ttt	gag	624				
Asp	Trp	Glu	Pro	Ile	Arg	Ser	Leu	Lys	Ser	Arg	Phe	Lys	Glu	Phe	Glu					
195					200					205										
aaa	cga	agc	tcg	tta	gaa	ata	ttg	agt	gga	ttc	aag	aac	agt	gaa	ttt	672				
Lys	Arg	Ser	Ser	Leu	Glu	Ile	Leu	Ser	Gly	Phe	Lys	Asn	Ser	Glu	Phe					
210					215					220										
gtt	gag	aag	ctc	aaa	acc	agc	ttt	aaa	tca	att	tac	aaa	gaa	act	gat	720				
Val	Glu	Lys	Leu	Lys	Thr	Ser	Phe	Lys	Ser	Ile	Tyr	Lys	Glu	Thr	Asp					
225					230					235					240					
gag	gct	aag	gat	gtc	cct	ccg	ttg	gat	gta	cct	gaa	ctg	ttg	gca	tgt	768				
Glu	Ala	Lys	Asp	Val	Pro	Pro	Leu	Asp	Val	Pro	Glu	Leu	Leu	Ala	Cys					
245					250					255										
ttg	gtt	aga	caa	tct	gaa	cct	ttt	ctt	gat	cag	att	ggg	gtt	aga	aag	816				
Leu	Val	Arg	Gln	Ser	Glu	Pro	Phe	Leu	Asp	Gln	Ile	Gly	Val	Arg	Lys					
260					265					270										
gat	aca	tgt	gac	cga	ata	gta	gaa	agc	ctt	tgc	aaa	tgc	aag	agc	caa	864				
Asp	Thr	Cys	Asp	Arg	Ile	Val	Glu	Ser	Leu	Cys	Lys	Cys	Lys	Ser	Gln					



275	280	285	
caa ctt tgg cgt ctg cca tct gca caa gca tcc gat tta att gaa aat Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn 290 295 300			912
gat aac cat gga gtt gat ttg gat atg agg ata gcc agt gtt ctt caa Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln 305 310 315 320			960
agc aca gga cac cat tat gat ggt ggg ttt tgg act gat ttt gtg aag Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys 325 330 335			1008
cct gag aca ccg gaa aac aaa agg cat gtg gca att gtt aca aca gct Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala 340 345 350			1056
agt ctt cct tgg atg acc gga aca gct gta aat ccg cta ttc aga gcg Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala 355 360 365			1104
gcg tat ttg gca aaa gct gca aaa cag agt gtt act ctc gtg gtt cct Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro 370 375 380			1152
tgg ctc tgc gaa tct gat caa gaa cta gtg tat cca aac aat ctc acc Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr 385 390 395 400			1200
ttc agc tca cct gaa gaa caa gag agt tat ata cgt aaa tgg ttg gag Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu 405 410 415			1248
gaa agg att ggt ttc aag gct gat ttt aaa atc tcc ttt tac cca gga Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly 420 425 430			1296
aag ttt tca aaa gaa agg cgc agc ata ttt cct gct ggt gac act tct Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser 435 440 445			1344
caa ttt ata tcg tca aaa gat gct gac att gct ata ctt gaa gaa cct Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro 450 455 460			1392
gaa cat ctc aac tgg tat tat cac ggc aag cgt tgg act gat aaa ttc Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe 465 470 475 480			1440
aac cat gtt gtt gga att gtc cac aca aac tac tta gag tac atc aag Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys 485 490 495			1488
agg gag aag aat gga gct ctt caa gca ttt ttt gtg aac cat gta aac Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn 500 505 510			1536
aat tgg gtc aca cga gcg tat tgt gac aag gtt ctt cgc ctc tct gcg Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala			1584

515					520					525							
gca	aca	caa	gat	tta	cca	aag	tct	gtt	gta	tgc	aat	gtc	cat	ggg	gtc	1632	
Ala	Thr	Gln	Asp	Leu	Pro	Lys	Ser	Val	Val	Cys	Asn	Val	His	Gly	Val		
530					535					540							
aat	ccc	aag	ttc	ctt	atg	att	ggg	gag	aaa	att	gct	gaa	gag	aga	tcc	1680	
Asn	Pro	Lys	Phe	Leu	Met	Ile	Gly	Glu	Lys	Ile	Ala	Glu	Glu	Arg	Ser		
545					550					555					560		
cgt	ggg	gaa	caa	gct	ttc	tca	aaa	ggg	gca	tac	ttc	tta	gga	aaa	atg	1728	
Arg	Gly	Glu	Gln	Ala	Phe	Ser	Lys	Gly	Ala	Tyr	Phe	Leu	Gly	Lys	Met		
565					570					575							
gtg	tgg	gct	aaa	gga	tac	aga	gaa	cta	ata	gat	ctg	atg	gct	aaa	cac	1776	
Val	Trp	Ala	Lys	Gly	Tyr	Arg	Glu	Leu	Ile	Asp	Leu	Met	Ala	Lys	His		
580					585					590							
aaa	agc	gaa	ctt	ggg	agc	ttc	aat	cta	gat	gta	tat	ggg	aac	ggg	gaa	1824	
Lys	Ser	Glu	Leu	Gly	Ser	Phe	Asn	Leu	Asp	Val	Tyr	Gly	Asn	Gly	Glu		
595					600					605							
gat	gca	gtc	gag	gtc	caa	cgt	gca	gca	aag	aaa	cat	gac	ttg	aat	ctc	1872	
Asp	Ala	Val	Glu	Val	Gln	Arg	Ala	Ala	Lys	Lys	His	Asp	Leu	Asn	Leu		
610					615					620							
aat	ttc	ctc	aaa	gga	agg	gac	cac	gct	gac	gat	gct	ctt	cac	aag	tac	1920	
Asn	Phe	Leu	Lys	Gly	Arg	Asp	His	Ala	Asp	Asp	Ala	Leu	His	Lys	Tyr		
625					630					635					640		
aaa	gtg	ttc	ata	aac	ccc	agc	atc	agc	gat	gtt	cta	tgc	aca	gca	acc	1968	
Lys	Val	Phe	Ile	Asn	Pro	Ser	Ile	Ser	Asp	Val	Leu	Cys	Thr	Ala	Thr		
645					650					655							
gca	gaa	gca	cta	gcc	atg	ggg	aag	ttt	gtg	gtg	tgt	gca	gat	cac	cct	2016	
Ala	Glu	Ala	Leu	Ala	Met	Gly	Lys	Phe	Val	Val	Cys	Ala	Asp	His	Pro		
660					665					670							
tca	aac	gaa	ttc	ttt	aga	tca	ttc	ccg	aac	tgc	tta	act	tac	aaa	aca	2064	
Ser	Asn	Glu	Phe	Phe	Arg	Ser	Phe	Pro	Asn	Cys	Leu	Thr	Tyr	Lys	Thr		
675					680					685							
tcc	gaa	gac	ttt	gtg	tcc	aaa	gtg	caa	gaa	gca	atg	acg	aaa	gag	cca	2112	
Ser	Glu	Asp	Phe	Val	Ser	Lys	Val	Gln	Glu	Ala	Met	Thr	Lys	Glu	Pro		
690					695					700							
cta	cct	ctc	act	cct	gaa	caa	atg	tac	aat	ctc	tct	tgg	gaa	gca	gca	2160	
Leu	Pro	Leu	Thr	Pro	Glu	Gln	Met	Tyr	Asn	Leu	Ser	Trp	Glu	Ala	Ala		
705					710					715					720		
aca	cag	agg	ttc	atg	gag	tat	tca	gat	ctc	gat	aag	atc	tta	aac	aat	2208	
Thr	Gln	Arg	Phe	Met	Glu	Tyr	Ser	Asp	Leu	Asp	Lys	Ile	Leu	Asn	Asn		
725					730					735							
gga	gag	gga	gga	agg	aag	atg	cga	aaa	tca	aga	tcg	gtt	ccg	agc	ttt	2256	
Gly	Glu	Gly	Gly	Arg	Lys	Met	Arg	Lys	Ser	Arg	Ser	Val	Pro	Ser	Phe		
740					745					750							
aac	gag	gtg	gtc	gat	gga	gga	ttg	gca	ttc	tca	cac	tat	gtt	cta	aca	2304	
Asn	Glu	Val	Val	Asp	Gly	Gly	Leu	Ala	Phe	Ser	His	Tyr	Val	Leu	Thr		

755	760	765	
ggg aac gat ttc ttg aga cta tgc act gga gca aca cca aga aca aaa			2352
Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys			
770	775	780	
gac tat gat aat caa cat tgc aag gat ctg aat ctc gta cca cct cac			2400
Asp Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His			
785	790	795	800
gtt cac aag cca atc ttc ggc tgg tag			2427
Val His Lys Pro Ile Phe Gly Trp			
805			

&lt;210&gt; 42

&lt;211&gt; 808

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 42

Met Val Lys Glu Thr Leu Ile Pro Pro Ser Ser Thr Ser Met Thr Thr
1 5 10 15

Gly Thr Ser Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn
20 25 30

Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala
35 40 45

Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn
50 55 60

Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser
65 70 75 80

Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser
85 90 95

Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe
100 105 110

Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg
115 120 125

Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys
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130	135	140
Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu		
145	150	155 160
Glu Met Ser Arg Leu Arg Arg Arg Arg Asn Ser Asp Arg Val Arg Phe		
	165	170 175
Thr Glu Phe Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly		
	180	185 190
Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu		
	195	200 205
Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe		
	210	215 220
Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp		
	225	230 235 240
Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys		
	245	250 255
Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys		
	260	265 270
Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln		
	275	280 285
Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn		
	290	295 300
Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln		
	305	310 315 320
Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys		
	325	330 335
Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala		
	340	345 350
Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala		
	355	360 365
Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro		

370	375	380
Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr		
385	390	395 400
Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu		
	405	410 415
Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly		
	420	425 430
Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser		
	435	440 445
Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro		
	450	455 460
Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe		
465	470	475 480
Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys		
	485	490 495
Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn		
	500	505 510
Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala		
	515	520 525
Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val		
	530	535 540
Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser		
545	550	555 560
Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met		
	565	570 575
Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His		
	580	585 590
Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu		
	595	600 605
Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu		

610					615					620					
Asn	Phe	Leu	Lys	Gly	Arg	Asp	His	Ala	Asp	Asp	Ala	Leu	His	Lys	Tyr
625					630					635					640
Lys	Val	Phe	Ile	Asn	Pro	Ser	Ile	Ser	Asp	Val	Leu	Cys	Thr	Ala	Thr
				645					650					655	
Ala	Glu	Ala	Leu	Ala	Met	Gly	Lys	Phe	Val	Val	Cys	Ala	Asp	His	Pro
			660					665					670		
Ser	Asn	Glu	Phe	Phe	Arg	Ser	Phe	Pro	Asn	Cys	Leu	Thr	Tyr	Lys	Thr
		675					680					685			
Ser	Glu	Asp	Phe	Val	Ser	Lys	Val	Gln	Glu	Ala	Met	Thr	Lys	Glu	Pro
	690					695					700				
Leu	Pro	Leu	Thr	Pro	Glu	Gln	Met	Tyr	Asn	Leu	Ser	Trp	Glu	Ala	Ala
705					710					715					720
Thr	Gln	Arg	Phe	Met	Glu	Tyr	Ser	Asp	Leu	Asp	Lys	Ile	Leu	Asn	Asn
				725					730					735	
Gly	Glu	Gly	Gly	Arg	Lys	Met	Arg	Lys	Ser	Arg	Ser	Val	Pro	Ser	Phe
			740					745					750		
Asn	Glu	Val	Val	Asp	Gly	Gly	Leu	Ala	Phe	Ser	His	Tyr	Val	Leu	Thr
		755					760					765			
Gly	Asn	Asp	Phe	Leu	Arg	Leu	Cys	Thr	Gly	Ala	Thr	Pro	Arg	Thr	Lys
	770					775					780				
Asp	Tyr	Asp	Asn	Gln	His	Cys	Lys	Asp	Leu	Asn	Leu	Val	Pro	Pro	His
785					790					795					800
Val	His	Lys	Pro	Ile	Phe	Gly	Trp								
				805											

<210> 43

<211> 1299

<212> DNA

<213> Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1299)

&lt;223&gt; 23915

&lt;400&gt; 43

atg gga gct agg gtt caa gta caa cat tac aat tta gga tca tct gat	48
Met Gly Ala Arg Val Gln Val Gln His Tyr Asn Leu Gly Ser Ser Asp	
1 5 10 15	
tcc tac atc gct act tct ctc cac gat ctc aac tcc gtc gat ggt ccg	96
Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro	
20 25 30	
ccg aga gat atc gac ggt atc gga ggc gcc gtt ggt cgt gac ggc gat	144
Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp	
35 40 45	
agt tta gat aat gac ggc gat tcc tct tct gcg gac tgt atg cat gaa	192
Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu	
50 55 60	
tca tac aga aac tct atg caa atc gga gta gaa gaa ggt gga tct aac	240
Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Gly Ser Asn	
65 70 75 80	
atg gag aac aaa gga tct gct tac att atg tta aac att gaa gat gtt	288
Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val	
85 90 95	
tca ccg att gaa gca gca aga ggg agg ttt ctg caa atc ata ttg gac	336
Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp	
100 105 110	
tac ttt att agc caa cat gtg att gaa gtc tgt gag agc aaa cgt gat	384
Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp	
115 120 125	
cat gat gtg gat tca gga gga cgt gat agt aat agt aaa gtg aag agg	432
His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg	
130 135 140	
aag tcg gat gat acg cga tat gaa ggt gat ccg agt ttt gcg tta ccg	480
Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro	
145 150 155 160	
ttg atg tat att gca aat ttg tat gag act tta gtt ggt gaa gca aat	528
Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn	
165 170 175	
gtg agg ctt gct tca ttg aat gga ata agg gat aag act att gga gta	576
Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val	
180 185 190	

gct ctt gaa gct gct ggt ggc ttg tat agg aaa tta act aag aag ttt Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe 195 200 205	624
cct aag aaa ggt act tgc atg tac agg aga aga gaa ctg gca act tca Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser 210 215 220	672
gtt gaa aca agg aca aga ttt cca gaa ttg gta ata cat gaa gag aaa Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys 225 230 235 240	720
cga gtt cgc ttt gtg gtg gtt aat ggt ttg gat att gtt gaa aag cca Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro 245 250 255	768
agt gat ttg cct att gaa gaa gct gaa tgg ttt aag cga tta aca ggc Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly 260 265 270	816
cgt aat gaa gtg gct atc tct gct aga gat tat aaa ttc tac tgc cct Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro 275 280 285	864
cga cgc aag cat agg cgt ctt cag aat tct gtc tcc agc atc aat ggc Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly 290 295 300	912
ttg cct aca ttt cca ggt ata gac tct tca acg tta gct aat aca caa Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln 305 310 315 320	960
gga ttt cgc gaa gat caa agc caa caa caa cac act cct tct cct tcc Gly Phe Arg Glu Asp Gln Ser Gln Gln Gln His Thr Pro Ser Pro Ser 325 330 335	1008
aaa cat cat atg tca tct ttg tct cat caa ttt cat caa tct att cac Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His 340 345 350	1056
cag agc cac caa cac cat caa tct ata tac caa agt caa cac gca gcc Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala 355 360 365	1104
aca cac tat ccc agt cag aac cat caa tgt gac cct gaa cta tct cac Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His 370 375 380	1152
aca caa atg gct tgc ttg caa ccc ctc act gga ggc cat gta atg cca Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro 385 390 395 400	1200
aat agt ccg gcg aaa ttt tgt gac caa tgt gga gca cag tac ttg aga Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg 405 410 415	1248
gag aca tcc aaa ttc tgc tca gag tgt ggt tcc aag aga ctc ggg ata Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile 420 425 430	1296



tag

1299

&lt;210&gt; 44

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 44

Met Gly Ala Arg Val Gln Val Gln His Tyr Asn Leu Gly Ser Ser Asp  
 1 5 10 15

Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro  
 20 25 30

Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp  
 35 40 45

Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu  
 50 55 60

Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Gly Ser Asn  
 65 70 75 80

Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val  
 85 90 95

Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp  
 100 105 110

Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp  
 115 120 125

His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg  
 130 135 140

Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro  
 145 150 155 160

Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn  
 165 170 175

Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val  
 180 185 190

Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe  
 195 200 205

Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser  
 210 215 220

Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys  
 225 230 235 240

Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro  
 245 250 255

Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly  
 260 265 270

Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro  
 275 280 285

Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly  
 290 295 300

Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln  
 305 310 315 320

Gly Phe Arg Glu Asp Gln Ser Gln Gln Gln His Thr Pro Ser Pro Ser  
 325 330 335

Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His  
 340 345 350

Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala  
 355 360 365

Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His  
 370 375 380

Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro  
 385 390 395 400

Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg  
 405 410 415

Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile  
 420 425 430

<210> 45

<211> 1617

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1617)

<223> 30945

<400> 45

atg aat gag gac aaa aat cct gct agg gct att gac ttg gct gcc agt 48  
 Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser  
 1 5 10 15

aat agc atg tat tta cgt gag acc ata ctt tct agt gaa tct cct agt 96  
 Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser  
 20 25 30

ctc aac act cag aat atc tca gtg aca gtt gaa atg cca ccc atg ttg 144  
 Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu  
 35 40 45

aaa ccg ttg cat ggg cat ctt ctt aaa cac ttt att gtg ttt tca aat 192  
 Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn  
 50 55 60

att gaa gac cag aac agt atc atc ata ata att cat gct act aac aat 240  
 Ile Glu Asp Gln Asn Ser Ile Ile Ile Ile Ile His Ala Thr Asn Asn  
 65 70 75 80

tgt cta cag cgt tgc ccg tca gtt act aaa gaa cag tgg gca gtg cca 288  
 Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro  
 85 90 95

gcg att ttg tct tct ttg aaa atg gaa gaa aac ctt ttg gcc cag gaa 336  
 Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu  
 100 105 110

agg gcc tgt gtg ttc ctc tcc ttg ttg ctg cat aac ttc tcc atg gtt 384  
 Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val  
 115 120 125

cac aca aca aaa act ggg aat act ctg aat gtt gat tct ttc tcc tgc 432  
 His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys  
 130 135 140

ttg gat tct ttc tca aag cat ata cgt ggt ggt atg gct gat act gaa Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu 145 150 155 160	480
gct gga gtt atg ctt tct gga ttt tcg gaa gaa ctc ctt tgt ctt ctt Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu 165 170 175	528
cag gac ctc ctt tct ggg cag cgg gta tta ttt tcg gtt aaa tcc tca Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser 180 185 190	576
gaa aca tgt gaa tct gat tta agc atc cct gtc acc ctg aat gga gaa Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu 195 200 205	624
aat gta gct ctc gtc aac aaa atc gct cta act gat caa ttg gtg gcc Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala 210 215 220	672
gga agc gct att ttg gcg gca ata tgt act gca ctt gat cgt att gga Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly 225 230 235 240	720
tat atc tgc gaa gct tcc ttt gaa atc ctg cac aag tac agt cat gag Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu 245 250 255	768
aaa acc tca gtg cta ctg acc att ctt cac gtt ttt gct tac att gct Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala 260 265 270	816
gga gag aaa atg gtg ttg tct agt gag cat ggc ata tca att gca gtg Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val 275 280 285	864
ttg aaa tac att gtc atg ttt cta gaa aac aaa cat ttt ggt act gtg Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val 290 295 300	912
gag ggc agt tct cga ttg cac cca ggc aag aac aag tgt cca ttc tca Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser 305 310 315 320	960
gac agg tct tcc tcg ctg gag gct atg gca tct aag ctc atg gaa att Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile 325 330 335	1008
ctt cag gaa ttt act gag tct aat act ttg cat aaa agc ttg act ggt Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly 340 345 350	1056
tca ttg ggt tct agc cac cta gag aag acc gag ttt agg ccg gca cac Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His 355 360 365	1104
aaa gat ttc cag tgt gta ttg acc agg gat caa agt atc aat ctc tgt Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys 370 375 380	1152

gac att cta tca ttg gtg gag ctt att gct tgt tat acg gct tgg gat 1200  
 Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp  
 385 390 395 400  
 tgg act agt gcg aac att gtt gct cca ctg ctt aag atg ctg gga atg 1248  
 Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met  
 405 410 415  
 cca ttg cca atg aac ctc tct gtt gca atc gtc tcc ctt ctt ggg caa 1296  
 Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln  
 420 425 430  
 ctt agc agt att gga gtg gat gct ggt ggc tat gaa aac gaa gga atc 1344  
 Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile  
 435 440 445  
 tca aac ttg aga gtg aaa ctg tca gca ttt cta cag tgt gag acg aca 1392  
 Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr  
 450 455 460  
 cta aag gcc ggt ttt gca gtg cag ata gca act gtg agc tcc ctc ctg 1440  
 Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu  
 465 470 475 480  
 aag acg ctg cag ctg aaa ttc cca ata gac ttt caa gac aaa acc acc 1488  
 Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr  
 485 490 495  
 atg att ccg ggt agt ggc gac caa agc tta tct ggt tca gtc aat gtg 1536  
 Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val  
 500 505 510  
 gtg acc aag tgg ttg tcg ttg ttg agc aag gaa caa cga gtt ttc gca 1584  
 Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala  
 515 520 525  
 ttt gag ttt cta caa acc aat gtt gtt aga tga 1617  
 Phe Glu Phe Leu Gln Thr Asn Val Val Arg  
 530 535

&lt;210&gt; 46

&lt;211&gt; 538

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 46

Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser  
 1 5 10 15

Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser  
 20 25 30

Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu  
 35 40 45

Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn  
 50 55 60

Ile Glu Asp Gln Asn Ser Ile Ile Ile Ile Ile His Ala Thr Asn Asn  
 65 70 75 80

Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro  
 85 90 95

Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu  
 100 105 110

Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val  
 115 120 125

His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys  
 130 135 140

Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu  
 145 150 155 160

Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu  
 165 170 175

Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser  
 180 185 190

Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu  
 195 200 205

Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala  
 210 215 220

Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly  
 225 230 235 240

Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu  
 245 250 255

Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala  
 260 265 270

Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val  
 275 280 285

Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val  
 290 295 300

Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser  
 305 310 315 320

Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile  
 325 330 335

Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly  
 340 345 350

Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His  
 355 360 365

Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys  
 370 375 380

Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp  
 385 390 395 400

Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met  
 405 410 415

Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln  
 420 425 430

Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile  
 435 440 445

Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr  
 450 455 460

Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu  
 465 470 475 480

Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr  
 485 490 495

Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val  
 500 505 510

Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala  
 515 520 525

Phe Glu Phe Leu Gln Thr Asn Val Val Arg  
 530 535

<210> 47

<211> 1332

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1332)

<223> 31895

<400> 47  
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 Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe  
 1 5 10 15  
 tca cca aaa agt gta cct ttt gct att cat agc gta acc agg agg caa 96  
 Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln  
 20 25 30  
 ttt ctt aat ccc aac acg ttt tat aga ttt ggg ttc tct cct tct ctt 144  
 Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu  
 35 40 45  
 cag gga agt agc att gag ttt agc ctt cag ttg aat tca aga gtt gtg 192  
 Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val  
 50 55 60  
 ctt agt aaa gag cgt cga tct ctg cca tta gtt gtg aga aat gat cgt 240  
 Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg  
 65 70 75 80  
 cct cag aat gaa gac tta cct aag cag tac aca agg cga gag aag aaa 288  
 Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys  
 85 90 95  
 cct ttc cca gtc cct att gtg gac ctg aga cga gct gcg agg gag aga 336  
 Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg  
 100 105 110  
 gtc aag aac aac aaa gac aaa cct aag aga cct cta cct ccg cct aaa 384



Val	Lys	Asn	Asn	Lys	Asp	Lys	Pro	Lys	Arg	Pro	Leu	Pro	Pro	Pro	Lys	
		115					120					125				
aat	ggt	atg	gtt	gtg	aag	agc	ctt	gtg	cct	ctt	gct	tat	aaa	gta	tac	432
Asn	Gly	Met	Val	Val	Lys	Ser	Leu	Val	Pro	Leu	Ala	Tyr	Lys	Val	Tyr	
		130				135					140					
aat	gca	aga	atc	aga	ttg	atc	aac	aat	ctc	cac	cgg	ctt	atg	aaa	gtt	480
Asn	Ala	Arg	Ile	Arg	Leu	Ile	Asn	Asn	Leu	His	Arg	Leu	Met	Lys	Val	
		145			150					155					160	
gtt	cgt	gtt	aat	gct	tgt	ggg	tgg	tgc	aat	gag	att	cat	gtt	gga	cct	528
Val	Arg	Val	Asn	Ala	Cys	Gly	Trp	Cys	Asn	Glu	Ile	His	Val	Gly	Pro	
				165					170					175		
tat	ggg	cat	cca	ttt	aag	tcg	tgt	aaa	ggt	ccc	aat	act	tcc	caa	agg	576
Tyr	Gly	His	Pro	Phe	Lys	Ser	Cys	Lys	Gly	Pro	Asn	Thr	Ser	Gln	Arg	
			180					185					190			
aaa	ggt	ctt	cat	gaa	tgg	act	aac	tcg	gtt	att	gag	gac	gtt	att	gtt	624
Lys	Gly	Leu	His	Glu	Trp	Thr	Asn	Ser	Val	Ile	Glu	Asp	Val	Ile	Val	
		195					200					205				
cct	ctt	gaa	gcc	tat	cac	ctt	ttt	gac	cgc	ctt	ggc	aag	cgt	atc	cgt	672
Pro	Leu	Glu	Ala	Tyr	His	Leu	Phe	Asp	Arg	Leu	Gly	Lys	Arg	Ile	Arg	
		210				215					220					
cat	gat	gaa	aga	ttc	tcg	att	ccc	cga	gtt	cct	gct	gta	gtt	gag	ctc	720
His	Asp	Glu	Arg	Phe	Ser	Ile	Pro	Arg	Val	Pro	Ala	Val	Val	Glu	Leu	
		225			230					235					240	
tgc	att	cag	ggc	ggc	gtt	gaa	ata	ccc	gaa	ttt	cca	gca	aaa	agg	aga	768
Cys	Ile	Gln	Gly	Gly	Val	Glu	Ile	Pro	Glu	Phe	Pro	Ala	Lys	Arg	Arg	
			245					250						255		
aga	aaa	ccg	att	atc	cgc	att	ggc	aaa	agc	gag	ttt	gtt	gat	gca	gat	816
Arg	Lys	Pro	Ile	Ile	Arg	Ile	Gly	Lys	Ser	Glu	Phe	Val	Asp	Ala	Asp	
		260						265					270			
gaa	act	gaa	ttg	cct	gat	cca	gag	cct	cag	cct	cct	cca	gtg	cca	ttg	864
Glu	Thr	Glu	Leu	Pro	Asp	Pro	Glu	Pro	Gln	Pro	Pro	Pro	Val	Pro	Leu	
		275				280						285				
tta	act	gag	tta	cct	gtc	tca	gag	atc	act	ccc	cca	tct	agc	gaa	gaa	912
Leu	Thr	Glu	Leu	Pro	Val	Ser	Glu	Ile	Thr	Pro	Pro	Ser	Ser	Glu	Glu	
		290				295					300					
gaa	aca	gtc	tcc	tta	gcc	gaa	gaa	aca	tta	cag	gcc	tgg	gaa	gaa	atg	960
Glu	Thr	Val	Ser	Leu	Ala	Glu	Glu	Thr	Leu	Gln	Ala	Trp	Glu	Glu	Met	
		305			310					315					320	
aga	gca	gga	gcc	aaa	aag	ctg	atg	agg	atg	tac	agg	gtt	agg	gtc	tgt	1008
Arg	Ala	Gly	Ala	Lys	Lys	Leu	Met	Arg	Met	Tyr	Arg	Val	Arg	Val	Cys	
			325					330					335			
ggg	tac	tgt	cca	gag	gtt	cac	gta	ggg	cca	acg	gga	cac	aag	gcc	cag	1056
Gly	Tyr	Cys	Pro	Glu	Val	His	Val	Gly	Pro	Thr	Gly	His	Lys	Ala	Gln	
			340					345					350			
aac	tgt	ggg	gca	ttc	aag	cac	caa	cag	cgg	aat	ggc	cag	cat	ggg	tgg	1104

Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp  
 355 360 365  
 caa tct gca gta ctt gac gac ttg ata ccg cca aga tat gtt tgg cat 1152  
 Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His  
 370 375 380  
 gtt cct gat gtg aat ggg cca ccg atg cag cga gag cta cga agc ttc 1200  
 Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe  
 385 390 395 400  
 tac ggg caa gca cct gct gtt gtg gag ata tgt gct cag gct ggc gct 1248  
 Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala  
 405 410 415  
 gtt gta cct gag cat tat aga gct aca atg aga ctg gag gtt gga att 1296  
 Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile  
 420 425 430  
 cct tcg agt gtg aaa gaa gct gag atg gtt gtt tga 1332  
 Pro Ser Ser Val Lys Glu Ala Glu Met Val Val  
 435 440

&lt;210&gt; 48

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe  
 1 5 10 15  
 Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln  
 20 25 30  
 Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu  
 35 40 45  
 Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val  
 50 55 60  
 Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg  
 65 70 75 80  
 Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys  
 85 90 95

Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg  
 100 105 110

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys  
 115 120 125

Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr  
 130 135 140

Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val  
 145 150 155 160

Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro  
 165 170 175

Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg  
 180 185 190

Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val  
 195 200 205

Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg  
 210 215 220

His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu  
 225 230 235 240

Cys Ile Gln Gly Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg  
 245 250 255

Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp  
 260 265 270

Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Pro Val Pro Leu  
 275 280 285

Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu  
 290 295 300

Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met  
 305 310 315 320

Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys  
 325 330 335

Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln  
 340 345 350

Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp  
 355 360 365

Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His  
 370 375 380

Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe  
 385 390 395 400

Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala  
 405 410 415

Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile  
 420 425 430

Pro Ser Ser Val Lys Glu Ala Glu Met Val Val  
 435 440

<210> 49

<211> 540

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (540)

<223> 34269

<400> 49  
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 Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln  
 1 5 10 15  
 tgt tgt tgt ttg aga gag atg atg gct gcg aag ctt cag aaa tgg cga 96  
 Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg  
 20 25 30  
 aat ctg gca ggt cgt cta gat ctg atg aat cgg agc ggc gct gtg tcg 144  
 Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser  
 35 40 45

acg agg cgg ttc ctg cac gaa ggt cca gat acc gtg gag gag ctt ctc 192  
 Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu  
 50 55 60

gaa aga cat cta gcg aag aaa gag aaa cca ata atc gat cac gat gag 240  
 Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu  
 65 70 75 80

gct gag ttt ctg aat aga cgg cgt ctg acg agc acg cgc cgg gaa gcg 288  
 Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala  
 85 90 95

ttg agt ttg tac aga gac ata tta cga gcg act cgg ttc ttc acg tgg 336  
 Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp  
 100 105 110

att gat tcc agg gga aat tta tgg agg gac gtg ttg aga gag aac gcg 384  
 Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala  
 115 120 125

agg aag gag ttt gaa gcg gcg cga ttt gag acg gat ccg gag gtt atc 432  
 Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile  
 130 135 140

aca agg ctt ctg ata ggt gga agc gac gcc gtt tcg tct gct tta gat 480  
 Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp  
 145 150 155 160

aag ctt gcg gag aag caa aga gag atg att gag aaa caa cgc cgt ggt 528  
 Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly  
 165 170 175

gat caa cgc tga 540  
 Asp Gln Arg

<210> 50

<211> 179

<212> PRT

<213> Arabidopsis thaliana

<400> 50

Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln  
 1 5 10 15

Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg  
 20 25 30

Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser  
 35 40 45

Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu  
 50 55 60  
 Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu  
 65 70 75 80  
 Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala  
 85 90 95  
 Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp  
 100 105 110  
 Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala  
 115 120 125  
 Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile  
 130 135 140  
 Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp  
 145 150 155 160  
 Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly  
 165 170 175  
 Asp Gln Arg

<210> 51

<211> 708

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(708)

<223> 34540

<400> 51

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48

Met	Arg	Ser	Pro	Arg	Thr	Leu	Glu	Val	Trp	Lys	Leu	Gly	Thr	Val	Asn	
1				5					10					15		
tat	ttg	aaa	tcc	ctt	aaa	ctg	cag	gag	aaa	tta	gtt	tca	gag	aga	aaa	96
Tyr	Leu	Lys	Ser	Leu	Lys	Leu	Gln	Glu	Lys	Leu	Val	Ser	Glu	Arg	Lys	
			20					25					30			
gct	cat	cag	att	cca	gat	acc	ctc	ctc	tcg	ctt	cag	cat	cca	cca	act	144
Ala	His	Gln	Ile	Pro	Asp	Thr	Leu	Leu	Ser	Leu	Gln	His	Pro	Pro	Thr	
			35				40					45				
tat	acg	ctc	gga	aag	cgt	aga	acc	gat	cac	aat	cta	ctt	atc	cct	gaa	192
Tyr	Thr	Leu	Gly	Lys	Arg	Arg	Thr	Asp	His	Asn	Leu	Leu	Ile	Pro	Glu	
	50					55					60					
tct	gaa	ctt	aca	aaa	atc	gga	gct	gaa	ctt	cat	tat	act	caa	aga	gga	240
Ser	Glu	Leu	Thr	Lys	Ile	Gly	Ala	Glu	Leu	His	Tyr	Thr	Gln	Arg	Gly	
65					70					75					80	
gga	gac	atc	acc	ttc	cat	ggc	cct	cat	caa	gcc	atc	tta	tat	ccc	atc	288
Gly	Asp	Ile	Thr	Phe	His	Gly	Pro	His	Gln	Ala	Ile	Leu	Tyr	Pro	Ile	
				85					90					95		
att	tcc	tta	cgc	agc	att	ggt	ttt	ggt	gct	agg	aac	tac	gtg	gag	aca	336
Ile	Ser	Leu	Arg	Ser	Ile	Gly	Phe	Gly	Ala	Arg	Asn	Tyr	Val	Glu	Thr	
			100					105					110			
ttg	gag	cgg	tca	atg	atc	gag	ttt	gct	tcg	att	tat	ggc	gtg	aaa	gct	384
Leu	Glu	Arg	Ser	Met	Ile	Glu	Phe	Ala	Ser	Ile	Tyr	Gly	Val	Lys	Ala	
			115				120					125				
cga	gca	gga	aac	aaa	tgt	gag	act	ggg	ggt	tgg	ggt	ggg	gat	agg	aag	432
Arg	Ala	Gly	Asn	Lys	Cys	Glu	Thr	Gly	Val	Trp	Val	Gly	Asp	Arg	Lys	
			130				135				140					
atc	ggt	gct	att	ggg	ggt	agg	ata	tct	tct	gga	atc	act	agt	cat	ggt	480
Ile	Gly	Ala	Ile	Gly	Val	Arg	Ile	Ser	Ser	Gly	Ile	Thr	Ser	His	Gly	
145					150					155					160	
ttg	gcc	tta	aat	ata	gat	cct	gat	atg	aag	tac	ttt	gag	cac	att	gtg	528
Leu	Ala	Leu	Asn	Ile	Asp	Pro	Asp	Met	Lys	Tyr	Phe	Glu	His	Ile	Val	
				165					170					175		
cct	tgt	ggg	att	gct	gat	aaa	gaa	ggt	aca	tct	ttg	cga	aga	gag	acg	576
Pro	Cys	Gly	Ile	Ala	Asp	Lys	Glu	Val	Thr	Ser	Leu	Arg	Arg	Glu	Thr	
			180					185					190			
gat	act	ctg	ctt	cct	tca	gaa	gaa	gtg	att	cat	gaa	cag	ttg	ggt	tct	624
Asp	Thr	Leu	Leu	Pro	Ser	Glu	Glu	Val	Ile	His	Glu	Gln	Leu	Val	Ser	
			195				200					205				
tgt	tta	gcc	aaa	gcg	ttt	tct	tat	gat	gat	ggt	gtc	tgg	aag	gaa	gat	672
Cys	Leu	Ala	Lys	Ala	Phe	Ser	Tyr	Asp	Asp	Val	Val	Trp	Lys	Glu	Asp	
		210				215				220						
cct	tca	ctc	att	ttg	gac	acc	caa	gat	aaa	gaa	taa					708
Pro	Ser	Leu	Ile	Leu	Asp	Thr	Gln	Asp	Lys	Glu						
225					230				235							

&lt;210&gt; 52

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 52

Met Arg Ser Pro Arg Thr Leu Glu Val Trp Lys Leu Gly Thr Val Asn  
 1 5 10 15

Tyr Leu Lys Ser Leu Lys Leu Gln Glu Lys Leu Val Ser Glu Arg Lys  
 20 25 30

Ala His Gln Ile Pro Asp Thr Leu Leu Ser Leu Gln His Pro Pro Thr  
 35 40 45

Tyr Thr Leu Gly Lys Arg Arg Thr Asp His Asn Leu Leu Ile Pro Glu  
 50 55 60

Ser Glu Leu Thr Lys Ile Gly Ala Glu Leu His Tyr Thr Gln Arg Gly  
 65 70 75 80

Gly Asp Ile Thr Phe His Gly Pro His Gln Ala Ile Leu Tyr Pro Ile  
 85 90 95

Ile Ser Leu Arg Ser Ile Gly Phe Gly Ala Arg Asn Tyr Val Glu Thr  
 100 105 110

Leu Glu Arg Ser Met Ile Glu Phe Ala Ser Ile Tyr Gly Val Lys Ala  
 115 120 125

Arg Ala Gly Asn Lys Cys Glu Thr Gly Val Trp Val Gly Asp Arg Lys  
 130 135 140

Ile Gly Ala Ile Gly Val Arg Ile Ser Ser Gly Ile Thr Ser His Gly  
 145 150 155 160

Leu Ala Leu Asn Ile Asp Pro Asp Met Lys Tyr Phe Glu His Ile Val  
 165 170 175

Pro Cys Gly Ile Ala Asp Lys Glu Val Thr Ser Leu Arg Arg Glu Thr  
 180 185 190



Asp Thr Leu Leu Pro Ser Glu Glu Val Ile His Glu Gln Leu Val Ser  
 195 200 205

Cys Leu Ala Lys Ala Phe Ser Tyr Asp Asp Val Val Trp Lys Glu Asp  
 210 215 220

Pro Ser Leu Ile Leu Asp Thr Gln Asp Lys Glu  
 225 230 235

<210> 53

<211> 1473

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1473)

<223>

<400> 53  
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 Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu  
 1 5 10 15  
 cgt cac acc gcg att ttt cac ggc gga gtt gga gtt aga ttc aaa ttc 96  
 Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe  
 20 25 30  
 ctt cgc agc ttt tct cct ctc tca gca aga cga gat aat ccc gat gtc 144  
 Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val  
 35 40 45  
 tcc aga aaa ccc caa ccg agc aaa aat atg ctc aga gcg aag cac atc 192  
 Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile  
 50 55 60  
 ggt aaa aat tac tcc tcc tcc ttg tca cca gtt ctc tcg ccg gag cat 240  
 Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His  
 65 70 75 80  
 aaa cct tcg ctc tta gag tct caa gct att ggt act gtc gca aca gct 288  
 Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala  
 85 90 95  
 caa gcg aac ttt atg cgc gtc att gtt caa gat gta gct aat tct gtg 336  
 Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val  
 100 105 110

acg agt gat gat gat aat gat tct tca aag act ggt gtt gaa ttg ctt	384
Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu	
115 120 125	
tgt gtg gtg aga gct gtg ttg aag aaa ata cga agg aga gtt tta gtt	432
Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val	
130 135 140	
gga gat aag gtt ctt gtt gga tct att gat tgg gtt gat aga aga gga	480
Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly	
145 150 155 160	
atg att gag aat gtg ttt cat cga cgt tcg gag att ttg gat cca cct	528
Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro	
165 170 175	
gtt gcg aac gtt gat cat ttg ctt gtt ctt ttc tct ttg gat caa ccg	576
Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro	
180 185 190	
aaa ctt gag ccg ttt act ctt act agg ttc ttg gtg gaa gct gaa tct	624
Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser	
195 200 205	
act cgt att cca tta aca ctt gct ttg aat aaa act gaa ctc att agt	672
Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser	
210 215 220	
gaa gag gaa ttg gaa act tgg aag ata agg ttg cgt gga tgg aac tat	720
Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr	
225 230 235 240	
gaa cca ttg ttt tgt agt gtg gga act aaa gat gga ctt gat gat att	768
Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile	
245 250 255	
gcg ttt gtt ctg aga gat cag act tct gtg att gtt gga cct agt ggt	816
Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly	
260 265 270	
gtt gga aag tcg agt tta atc aac gta ttg agg agt aat cat ggt ggt	864
Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly	
275 280 285	
ggt gtg gtg gaa gat gag aat tgg ttt gag cct atg tta ggt aat aag	912
Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys	
290 295 300	
tgg ttt gat gat cag cga gta ggg gaa gtt tcg agt aga agt ggt aga	960
Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg	
305 310 315 320	
ggt aaa cat aca aca cga aat gta tcg cta ctg ccg gtt tct gaa ggt	1008
Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly	
325 330 335	
ggt tac ctc gct gat act cct ggc ttt aac cag cct agt ttg ctg aaa	1056
Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys	
340 345 350	

gta acg aag cat tca cta gct cac tgt ttt cct gag ata cgg aac atg 1104  
Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met  
355 360 365

att gag agc gaa aaa tgt gga ttc aga gac tgc ttg cat att ggg gaa 1152  
Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu  
370 375 380

cca gga tgt gtt gtg aaa ggt gac tgg gaa agg tat cct tac tac tta 1200  
Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu  
385 390 395 400

caa ttg ctt gat gag atc aga atc agg gaa gaa ttt cag ctt agg act 1248  
Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr  
405 410 415

ttt gga acc aaa agg gaa gat gat gtt agg tac aag gtg gga gac atg 1296  
Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met  
420 425 430

ggt gtg aaa cat gct gaa cca cgg tta atg cct aag aag cat agg aga 1344  
Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg  
435 440 445

gag tca agg aag aaa acg aaa cag aca atg atc agt gag ctg gat gag 1392  
Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu  
450 455 460

ttc gaa gat gaa gac agt gat ttg tac ata gag aac gac cca atc gtc 1440  
Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val  
465 470 475 480

caa gcc att gag aat gag aat aaa aga caa tga 1473  
Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln  
485 490

&lt;210&gt; 54

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 54

Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu  
1 5 10 15

Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe  
20 25 30

Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val  
35 40 45

Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile  
 50 55 60

Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His  
 65 70 75 80

Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala  
 85 90 95

Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val  
 100 105 110

Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu  
 115 120 125

Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val  
 130 135 140

Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly  
 145 150 155 160

Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro  
 165 170 175

Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro  
 180 185 190

Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser  
 195 200 205

Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser  
 210 215 220

Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr  
 225 230 235 240

Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile  
 245 250 255

Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly  
 260 265 270

Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly  
 275 280 285

Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys  
 290 295 300

Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg  
 305 310 315 320

Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly  
 325 330 335

Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys  
 340 345 350

Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met  
 355 360 365

Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu  
 370 375 380

Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu  
 385 390 395 400

Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr  
 405 410 415

Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met  
 420 425 430

Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg  
 435 440 445

Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu  
 450 455 460

Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val  
 465 470 475 480

Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln  
 485 490

<210> 55

<211> 897

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(897)

&lt;223&gt; 35154

&lt;400&gt; 55

atg	gtg	ttt	gga	caa	gta	gta	ata	ggg	cct	cca	gga	tcg	gga	aag	acc	48
Met	Val	Phe	Gly	Gln	Val	Val	Ile	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	
1			5					10					15			

act	tat	tgc	aat	gga	atg	tct	cag	ttc	ctc	tct	cta	atg	ggc	agg	aag	96
Thr	Tyr	Cys	Asn	Gly	Met	Ser	Gln	Phe	Leu	Ser	Leu	Met	Gly	Arg	Lys	
			20				25						30			

gtt	gct	att	gtt	aat	ctg	gat	cct	gca	aat	gat	gca	tta	cct	tat	gag	144
Val	Ala	Ile	Val	Asn	Leu	Asp	Pro	Ala	Asn	Asp	Ala	Leu	Pro	Tyr	Glu	
		35				40					45					

tgt	ggg	gtg	aat	ata	gaa	gaa	ttg	atc	aag	tta	gaa	gat	gtt	atg	tcg	192
Cys	Gly	Val	Asn	Ile	Glu	Glu	Leu	Ile	Lys	Leu	Glu	Asp	Val	Met	Ser	
	50					55					60					

gaa	cac	tcg	ctt	ggg	cct	aat	gga	ggg	ctt	gta	tat	tgt	atg	gag	tac	240
Glu	His	Ser	Leu	Gly	Pro	Asn	Gly	Gly	Leu	Val	Tyr	Cys	Met	Glu	Tyr	
65					70				75					80		

ttg	gag	aaa	aac	att	gac	tgg	ctg	gaa	tct	aaa	cta	aag	cct	ctt	ctg	288
Leu	Glu	Lys	Asn	Ile	Asp	Trp	Leu	Glu	Ser	Lys	Leu	Lys	Pro	Leu	Leu	
			85					90						95		

aag	gat	cat	tac	att	ctc	ttt	gat	ttt	cct	ggc	caa	gtg	gaa	ttg	ttc	336
Lys	Asp	His	Tyr	Ile	Leu	Phe	Asp	Phe	Pro	Gly	Gln	Val	Glu	Leu	Phe	
			100				105						110			

ttc	att	cat	gac	agt	acc	aag	aat	gtt	ctc	acg	aag	ctg	att	aaa	tca	384
Phe	Ile	His	Asp	Ser	Thr	Lys	Asn	Val	Leu	Thr	Lys	Leu	Ile	Lys	Ser	
		115					120					125				

ttg	aac	ctt	aga	tta	act	gct	gtg	caa	cta	att	gat	tcc	cat	cta	tgt	432
Leu	Asn	Leu	Arg	Leu	Thr	Ala	Val	Gln	Leu	Ile	Asp	Ser	His	Leu	Cys	
	130					135					140					

tgt	gat	ccc	ggg	aac	tac	gta	agt	tcg	cta	ctt	ctc	tcc	tta	tcc	aca	480
Cys	Asp	Pro	Gly	Asn	Tyr	Val	Ser	Ser	Leu	Leu	Leu	Ser	Leu	Ser	Thr	
145				150					155						160	

atg	ctt	cac	atg	gaa	ctc	cca	cat	gtc	aat	gta	ttg	tct	aaa	atc	gat	528
Met	Leu	His	Met	Glu	Leu	Pro	His	Val	Asn	Val	Leu	Ser	Lys	Ile	Asp	
				165					170					175		

ctg att gga agc tac ggg aag cta gct ttc aat tta gat ttc tat acc 576  
 Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr  
 180 185 190

gat gtt caa gac ttg tca tac ttg gag cac cat ctt agt caa gat cct 624  
 Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro  
 195 200 205

cgc tct gct aag tac aga aaa cta aca aaa gag cta tgt agt gtc att 672  
 Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile  
 210 215 220

gaa gat tac agt ctt gtt aat ttt aca acc ttg gat att cag gat aaa 720  
 Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys  
 225 230 235 240

gaa agt gtt ggg gat cta gta aag ctc atc gac aag agc aat gga tac 768  
 Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr  
 245 250 255

ata ttt gcc ggc att gat gca agt gtg gtt gaa tac agc aag att gca 816  
 Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala  
 260 265 270

att ggt caa act gat tgg gat tat aac aga gtc gca gct gta cag gag 864  
 Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu  
 275 280 285

aag tac atg gaa gat gag gaa ata caa gac tga 897  
 Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp  
 290 295

&lt;210&gt; 56

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 56

Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr  
1 5 10 15

Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys  
20 25 30

Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu  
35 40 45

Cys Gly Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser  
50 55 60

Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr  
65 70 75 80

Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu  
85 90 95

Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe  
100 105 110

Phe Ile His Asp Ser Thr Lys Asn Val Leu Thr Lys Leu Ile Lys Ser  
115 120 125

Leu Asn Leu Arg Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys  
130 135 140

Cys Asp Pro Gly Asn Tyr Val Ser Ser Leu Leu Leu Ser Leu Ser Thr  
145 150 155 160

Met Leu His Met Glu Leu Pro His Val Asn Val Leu Ser Lys Ile Asp  
165 170 175

Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr  
180 185 190

Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro  
195 200 205

Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile  
210 215 220

Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys  
225 230 235 240

Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr  
245 250 255

Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala  
260 265 270

Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu  
275 280 285

Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp  
290 295



&lt;210&gt; 57

&lt;211&gt; 849

&lt;212&gt; DNA

<213> *Arabidopsis thaliana*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (849)

&lt;223&gt; 35438

&lt;400&gt; 57

atg gaa gct ctc tac gcc aag ctc tac gac aaa tac acc aaa ctc cag	48
Met Glu Ala Leu Tyr Ala Lys Leu Tyr Asp Lys Tyr Thr Lys Leu Gln	
1 5 10 15	

aag aag aaa tat tcc gaa tac gat gag att aat aag gaa caa gaa gag	96
Lys Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu	
20 25 30	

aaa ttc ctt acc ttt gtt tca gcc tca gag gag ttg atg gaa cat ttg	144
Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu	
35 40 45	

aga ggt gaa aat cag agt tct ctg gag atg gtt gag aag ttg agg aat	192
Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn	
50 55 60	

gaa atc att tca atc aga tct ggc agg gac gac aag ttt ctg gag tgt	240
Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys	
65 70 75 80	

caa aag ctt ctc atg gaa gaa gaa cta aag aac aaa tca ctt tct gaa	288
Gln Lys Leu Leu Met Glu Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu	
85 90 95	

gaa gtt gtc aag cta aaa gag ctg gtc caa gag gaa cat cct cgc aac	336
Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn	
100 105 110	

tat gaa gat caa agt gga aaa aaa caa aag aga aag act cct gaa agt	384
Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser	
115 120 125	

gct cga gtt aca acg aga agc atg ata aaa cgt agc aga ctg tca gaa	432
Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu	
130 135 140	

gat ttg gtg gaa acg gat atg gta tca cct gac att agc aaa cat cat	480
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Asp	Leu	Val	Glu	Thr	Asp	Met	Val	Ser	Pro	Asp	Ile	Ser	Lys	His	His	
145					150					155					160	
aaa	gca	aag	gag	cct	ctc	ttg	gtt	tct	cag	cca	caa	tgc	tgc	aga	aca	528
Lys	Ala	Lys	Glu	Pro	Leu	Leu	Val	Ser	Gln	Pro	Gln	Cys	Cys	Arg	Thr	
				165					170					175		
acc	tac	gat	gga	tca	agt	agt	tct	gct	agt	tgt	aca	ttt	caa	gct	ctt	576
Thr	Tyr	Asp	Gly	Ser	Ser	Ser	Ser	Ala	Ser	Cys	Thr	Phe	Gln	Ala	Leu	
			180					185					190			
ggc	aaa	cac	ttg	cta	gga	atg	aaa	tta	tca	act	aat	aat	aag	ggc	aaa	624
Gly	Lys	His	Leu	Leu	Gly	Met	Lys	Leu	Ser	Thr	Asn	Asn	Lys	Gly	Lys	
		195					200					205				
cgc	gcc	tgc	att	gta	gcc	tca	cac	cca	aca	acc	ggg	tta	tcc	ttc	agc	672
Arg	Ala	Cys	Ile	Val	Ala	Ser	His	Pro	Thr	Thr	Gly	Leu	Ser	Phe	Ser	
		210				215					220					
cta	act	ttt	ata	aat	aac	cca	aat	ggg	gaa	gaa	tct	gag	ctg	ctt	tac	720
Leu	Thr	Phe	Ile	Asn	Asn	Pro	Asn	Gly	Glu	Glu	Ser	Glu	Leu	Leu	Tyr	
225					230				235						240	
aag	cct	gca	tca	ctc	gga	aca	ttt	caa	aga	gtg	gca	ccg	gaa	tgg	atg	768
Lys	Pro	Ala	Ser	Leu	Gly	Thr	Phe	Gln	Arg	Val	Ala	Pro	Glu	Trp	Met	
				245				250						255		
aga	gaa	gtt	ata	aag	ttc	agc	aca	agt	atg	tgt	ccc	atc	ttc	ttt	gaa	816
Arg	Glu	Val	Ile	Lys	Phe	Ser	Thr	Ser	Met	Cys	Pro	Ile	Phe	Phe	Glu	
			260					265					270			
aga	gtc	tct	cga	gtc	att	aag	ctc	aat	tgt	tga						849
Arg	Val	Ser	Arg	Val	Ile	Lys	Leu	Asn	Cys							
		275					280									

&lt;210&gt; 58

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 58

Met	Glu	Ala	Leu	Tyr	Ala	Lys	Leu	Tyr	Asp	Lys	Tyr	Thr	Lys	Leu	Gln
1				5					10					15	

Lys	Lys	Lys	Tyr	Ser	Glu	Tyr	Asp	Glu	Ile	Asn	Lys	Glu	Gln	Glu	Glu
			20					25					30		

Lys	Phe	Leu	Thr	Phe	Val	Ser	Ala	Ser	Glu	Glu	Leu	Met	Glu	His	Leu
		35					40					45			

Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn  
 50 55 60

Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys  
 65 70 75 80

Gln Lys Leu Leu Met Glu Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu  
 85 90 95

Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn  
 100 105 110

Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser  
 115 120 125

Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu  
 130 135 140

Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His  
 145 150 155 160

Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr  
 165 170 175

Thr Tyr Asp Gly Ser Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu  
 180 185 190

Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys  
 195 200 205

Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser  
 210 215 220

Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Glu Ser Glu Leu Leu Tyr  
 225 230 235 240

Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met  
 245 250 255

Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu  
 260 265 270

Arg Val Ser Arg Val Ile Lys Leu Asn Cys  
 275 280

&lt;210&gt; 59

&lt;211&gt; 1467

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1467)

&lt;223&gt; 37351

&lt;400&gt; 59

atg gaa ttg gat tcg gag aac aaa ttg ttg aag acg ggt ttg gtt ata	48
Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile	
1 5 10 15	

gtg gcg aca ctt gtt ata gcc aaa ctc atc ttc tct ttc ttc act tct	96
Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser	
20 25 30	

gat tct aag aag aag cgt ctt cct cct act ctt aaa gct tgg cct cca	144
Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro	
35 40 45	

ttg gtt gga agt ctt atc aaa ttc ttg aaa gga cct att att atg ctt	192
Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu	
50 55 60	

aga gag gaa tac cct aag ctt gga agt gtg ttt act gtt aat ctt gtt	240
Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val	
65 70 75 80	

cac aaa aag att act ttt ctt att ggt cct gaa gtc tct gct cat ttt	288
His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe	
85 90 95	

ttc aaa gct tct gaa tct gat ctt agt cag cag gaa gtg tat cag ttc	336
Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe	
100 105 110	

aat gtc cct act ttt ggt cct gga gtt gtt ttc gat gtt gat tat tct	384
Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser	
115 120 125	

gtt cgt cag gag cag ttt cgg ttc ttc act gag gca ctt aga gtt aac	432
Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn	
130 135 140	

aag ttg aag ggt tat gtg gat atg atg gtt act gaa gct gag gat tac	480
Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr	
145 150 155 160	

ttc tct aaa tgg gga gag agt ggt gaa gtt gat att aag gtt gag cta	528
Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu	
165 170 175	
gag agg ctc atc atc ttg act gca agt aga tgt tta ctg ggt cga gaa	576
Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu	
180 185 190	
gtt cgt gat cag ctt ttt gat gat gtc tct gct ttg ttc cat gac ctt	624
Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu	
195 200 205	
gac aat gga atg ctt ccc atc agt gtt ctc ttc cca tat ctc cca att	672
Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile	
210 215 220	
cca gct cac cgc cgt cgt gac cgt gcc cga gaa aag ctt tcg gag att	720
Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile	
225 230 235 240	
ttc gca aaa atc att ggg tcg aga aaa cgc tct gga aaa aca gag aac	768
Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn	
245 250 255	
gac atg ctg cag tgt ttc atc gaa tca aag tac aaa gat ggt aga cag	816
Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln	
260 265 270	
aca acc gaa tct gaa gtc act ggt ttg ctc att gct gct ctg ttt gca	864
Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala	
275 280 285	
gga caa cac acg agc tct atc act tcc acc tgg acc ggt gct tat ctg	912
Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu	
290 295 300	
atg cga tac aaa gag tac ttc tca gct gct ctt gat gag cag aag aac	960
Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn	
305 310 315 320	
ctg att gcg aaa cat gga gac aag atc gat cat gat atc tta tcc gag	1008
Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu	
325 330 335	
atg gat gtt ctc tac cgc tgc att aag gaa gcg ttg agg ctt cac cct	1056
Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro	
340 345 350	
cca ctc atc atg tta atg aga gcc tcg cac agt gat ttc agc gtg aca	1104
Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr	
355 360 365	
gct cgg gat gga aaa act tac gat atc cca aag ggt cac atc gtt gca	1152
Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala	
370 375 380	
acc tcc cct gca ttt gcc aac cgc tta ccg cac atc ttc aaa gac ccc	1200
Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro	
385 390 395 400	

gac acc tac gac cca gaa aga ttc tcc cct gga aga gaa gag gac aaa 1248  
 Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys  
 405 410 415  
  
 gcc gca ggg gca ttc tcg tac att gca ttc gga ggg gga agg cac ggg 1296  
 Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly  
 420 425 430  
  
 tgc ctt gga gag ccg ttt gct tac ctg cag atc aaa gcc ata tgg agt 1344  
 Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser  
 435 440 445  
  
 cat ttg ttg agg aac ttc gag ctt gag cta gtt tca ccg ttc cct gag 1392  
 His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu  
 450 455 460  
  
 att gac tgg aac gct atg gtg gtt gga gtt aaa ggc aat gtg atg gtg 1440  
 Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val  
 465 470 475 480  
  
 cgt tac aag agg cgc cag ctt tct taa 1467  
 Arg Tyr Lys Arg Arg Gln Leu Ser  
 485

&lt;210&gt; 60

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 60

Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile  
 1 5 10 15

Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser  
 20 25 30

Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro  
 35 40 45

Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu  
 50 55 60

Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val  
 65 70 75 80

His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe  
 85 90 95

Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe  
 100 105 110  
 Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser  
 115 120 125  
 Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn  
 130 135 140  
 Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr  
 145 150 155 160  
 Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu  
 165 170 175  
 Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu  
 180 185 190  
 Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu  
 195 200 205  
 Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile  
 210 215 220  
 Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile  
 225 230 235 240  
 Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn  
 245 250 255  
 Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln  
 260 265 270  
 Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala  
 275 280 285  
 Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu  
 290 295 300  
 Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn  
 305 310 315 320  
 Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu  
 325 330 335

Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro  
 340 345 350

Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr  
 355 360 365

Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala  
 370 375 380

Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro  
 385 390 395 400

Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys  
 405 410 415

Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly  
 420 425 430

Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser  
 435 440 445

His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu  
 450 455 460

Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val  
 465 470 475 480

Arg Tyr Lys Arg Arg Gln Leu Ser  
 485

<210> 61

<211> 1836

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1836)

<223> 37389



<400> 61  
 atg ggg att gtt ttg gaa cct cct tgt cct aaa agt gtt gat ggg att 48  
 Met Gly Ile Val Leu Glu Pro Pro Cys Pro Lys Ser Val Asp Gly Ile  
 1 5 10 15

agc att gat cct gag cct aat tgg aat ttc gag agt ttg gtc gct gag 96  
 Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu  
 20 25 30

att gct tct gtt gaa aag aag ctc aat ggc ttc tca atg tat cct cag 144  
 Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln  
 35 40 45

cca att act aac aca acc tta cgg atg gga agg aga ggt gga gga ttt 192  
 Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Gly Phe  
 50 55 60

gta atg cat gtc tca gaa gat gag atg gag agt gac gaa ggt gaa gag 240  
 Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu  
 65 70 75 80

agt gat gat gag gaa gaa gaa gaa gat cat agt caa atc tgt aca gcg 288  
 Ser Asp Asp Glu Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala  
 85 90 95

gga aaa cgt ttt gcc tgt gat gag ctt tac ttg agt gat gaa tct gat 336  
 Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp  
 100 105 110

gaa gag ttt gat cat gaa cct gag tat atg atg aat aag ttg ggt ctg 384  
 Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu  
 115 120 125

gct gag agt gcc cta tat gag gtt atc aac gac cac caa acc gaa atc 432  
 Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile  
 130 135 140

aag gac gac att agg aat caa gta tca gtt gtt gaa aca gaa ata atg 480  
 Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met  
 145 150 155 160

aat gag att gaa acg tct ctc tct gcc ata gcc cgg gtt gaa aag tac 528  
 Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr  
 165 170 175

agt gag act cgg aaa gaa gtt gaa cgg aaa ctt gat ctt caa tat cag 576  
 Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln  
 180 185 190

cga aaa gtt gct gaa gca ctt gat acc cat ctg act gca gtc caa cgc 624  
 Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg  
 195 200 205

gaa cat aaa att aaa tcg caa ata gaa gaa aga aag ata agg agc gag 672  
 Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu  
 210 215 220

gaa gct cag gag gag gcc agg agg aag gaa agg gct cat caa gaa gag 720

Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu 225 230 235 240	
aaa ata cgt caa gaa aaa gct cgc gca gag gct caa atg cta gca aaa Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys 245 250 255	768
atc aga gct gaa gaa gaa aag aaa gaa gtt gag aga aag gca gcc aga Ile Arg Ala Glu Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg 260 265 270	816
gaa gta gct gaa aaa gaa gta gca gat cgc aaa gct gcc gaa caa aaa Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys 275 280 285	864
ctt gcg gaa cag aag gct gtg ata gag agt gtt acg ggg agt tca gct Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala 290 295 300	912
aca tca aat gct caa gct ggg ggt aat tca atc cga gct gca gaa agt Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser 305 310 315 320	960
gct ttg ata ttg gag aac cac aga ttg aaa aag ctc gaa gaa cta gaa Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu 325 330 335	1008
aca acg aac caa tcg ctt aag tca cgt tca aat gaa aac ttt agc agt Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser 340 345 350	1056
ttt gag aag cat att gga aga gtg ata agg caa ata agt ggg aca aag Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys 355 360 365	1104
gat agt gta agt ggg aaa atc aat gat att gtg aaa ata ttt aaa gac Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp 370 375 380	1152
cct cgt tgt ccg gta tcc ata agt att gca gct ttt gca aag aag atg Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met 385 390 395 400	1200
gtc acc act aag gaa aaa cca aac cct ttt gca tgc agc tat gtc att Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile 405 410 415	1248
gtt tac atc aac tca cag ttt ccc caa gtt atg gat att ctt ctc gcg Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala 420 425 430	1296
gaa ttc cac aaa gct tgc att tac act gtc cca aag cat att gta aac Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn 435 440 445	1344
tca cag tca gct tgg gat tca gac gca tat gaa cgc cta gat tct ata Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile 450 455 460	1392
atg agg ctc tac ggt gca ctt gtt cag acc gat atc cgc gtt ggc aat	1440

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn  
 465 470 475 480

gct act aac gtt cat ggg ata gaa cat gga tgg gct tgg tta gcc cgg 1488  
 Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg  
 485 490 495

ttc ctt aac aaa atc cca gcc aac aga gcc act gcg aca gcc ttg aac 1536  
 Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn  
 500 505 510

tcc ttt ctc cag acg gct ggg ttt ggt ctt cat cag agg tac aaa tct 1584  
 Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser  
 515 520 525

cag ttt ctg aag gtt gtg aat gtt gtg aga gag cat ttc ttg cag aaa 1632  
 Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys  
 530 535 540

ttg cgg gcg aag aag gac acg tcg gat cta ctt gtg atc ata gcc gaa 1680  
 Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu  
 545 550 555 560

atc aca gcg tac tta gat gac cgg atg tat ctc aag gaa cct gaa gga 1728  
 Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly  
 565 570 575

aga gct atg aag acg act agt acc ttg tcc tct gaa ctt act gct gaa 1776  
 Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu  
 580 585 590

tta aat cag ccg aac tac aat cag aat tac cag agg aat gat tac aga 1824  
 Leu Asn Gln Pro Asn Tyr Asn Gln Asn Tyr Gln Arg Asn Asp Tyr Arg  
 595 600 605

aac tac tat tga 1836  
 Asn Tyr Tyr  
 610

&lt;210&gt; 62

&lt;211&gt; 611

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 62

Met Gly Ile Val Leu Glu Pro Pro Cys Pro Lys Ser Val Asp Gly Ile  
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Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu  
 20 25 30

Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln  
 35 40 45

Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Gly Phe  
 50 55 60

Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu  
 65 70 75 80

Ser Asp Asp Glu Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala  
 85 90 95

Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp  
 100 105 110

Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu  
 115 120 125

Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile  
 130 135 140

Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met  
 145 150 155 160

Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr  
 165 170 175

Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln  
 180 185 190

Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg  
 195 200 205

Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu  
 210 215 220

Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu  
 225 230 235 240

Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys  
 245 250 255

Ile Arg Ala Glu Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg  
 260 265 270

Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys  
 275 280 285

Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala  
 290 295 300

Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser  
 305 310 315 320

Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu  
 325 330 335

Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser  
 340 345 350

Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys  
 355 360 365

Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp  
 370 375 380

Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met  
 385 390 395 400

Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile  
 405 410 415

Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala  
 420 425 430

Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn  
 435 440 445

Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile  
 450 455 460

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn  
 465 470 475 480

Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg  
 485 490 495

Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn  
 500 505 510

Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser  
 515 520 525

Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys  
 530 535 540

Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu  
 545 550 555 560

Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly  
 565 570 575

Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu  
 580 585 590

Leu Asn Gln Pro Asn Tyr Asn Gln Asn Tyr Gln Arg Asn Asp Tyr Arg  
 595 600 605

Asn Tyr Tyr  
 610

<210> 63

<211> 1152

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1152)

<223> 38108

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tct tct ttc aaa act tct tct tct tct tca ttt tct ccg aag ctt ctt	96
Ser Ser Phe Lys Thr Ser Ser Ser Ser Ser Ser Phe Ser Pro Lys Leu Leu	
20 25 30	
cga ccc ctc tta agc ttt tcc gtc aaa gct tcc aga aag caa gta gag	144
Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu	
35 40 45	

ata gtg ttt gat cct gat gag agg ctt aat aag ata ggt gat gat gtt Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val 50 55 60	192
gac aaa gaa gct cct ttg tcc agg ctt aag ctc ttc tca cct tgc aag Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys 65 70 75 80	240
atc aat gtt ttc ttg agg atc acc gga aag cga gaa gat ggg ttt cat Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His 85 90 95	288
gat tta gcc tct ttg ttt cat gtg att agc tta gga gac act att aaa Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys 100 105 110	336
ttc tca ttg tca cca tca aag tct aaa gat cgt ttg tct act aac gtt Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val 115 120 125	384
caa gga gtc cct gtt gat ggg aga aat ctg att ata aaa gca ctt aac Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn 130 135 140	432
ctt tac agg aag aaa act ggt agt aac aga ttc ttc tgg att cat tta Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu 145 150 155 160	480
gat aag aag gtg cct acc ggg gct gga ctc ggt ggt gga agt agt aat Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Gly Ser Ser Asn 165 170 175	528
gct gca act gca ctc tgg gcg gca aat gag ctc aat gga ggt ctt gtc Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val 180 185 190	576
act gag aac gaa ctc cag gat tgg tca agt gaa att ggg tca gat att Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile 195 200 205	624
cct ttc ttc ttc tcg cat gga gct gcc tat tgt acc ggg aga ggt gag Pro Phe Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu 210 215 220	672
att gtc caa gac ctt cct cca cct ttt cct ctt gat ctt ccg atg gtg Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val 225 230 235 240	720
ctc ata aag ccc cga gaa gca tgt tcc act gct gaa gtt tac aaa cgt Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg 245 250 255	768
ctt cgt tta gat cag acg agc aat att aat ccc ttg aca tta cta gag Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu 260 265 270	816
aat gtg acc agc aat ggt gtg tct caa agc ata tgc gta aac gat ttg Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu 275 280 285	864

gaa ccg cca gcg ttt tca gtt ctt cca tct cta aaa cgc ttg aag caa 912  
 Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln  
 290 295 300  
 cgg ata ata gca tct gga cgt ggg gaa tac gat gct gtg ttt atg tct 960  
 Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser  
 305 310 315 320  
 ggg agt gga agc act att atc ggt att ggt tca cca gat cct cct caa 1008  
 Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln  
 325 330 335  
 ttt ata tat gat gat gaa gaa tac aag aac gtg ttc ttg tct gaa gca 1056  
 Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala  
 340 345 350  
 aac ttt atg acg cgt gag gct aat gaa tgg tac aaa gaa cct gct tct 1104  
 Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser  
 355 360 365  
 gca aat gct act acc tca tcc gcc gaa tct cgc atg gat ttc caa tga 1152  
 Ala Asn Ala Thr Thr Ser Ser Ala Glu Ser Arg Met Asp Phe Gln  
 370 375 380

<210> 64

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 64

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 20 25 30  
 Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu  
 35 40 45  
 Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val  
 50 55 60  
 Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys  
 65 70 75 80  
 Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His  
 85 90 95



Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys  
 100 105 110

Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val  
 115 120 125

Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn  
 130 135 140

Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu  
 145 150 155 160

Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Gly Ser Ser Asn  
 165 170 175

Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val  
 180 185 190

Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile  
 195 200 205

Pro Phe Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu  
 210 215 220

Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val  
 225 230 235 240

Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg  
 245 250 255

Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu  
 260 265 270

Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu  
 275 280 285

Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln  
 290 295 300

Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser  
 305 310 315 320

Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln  
 325 330 335

Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala  
 340 345 350

Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser  
 355 360 365

Ala Asn Ala Thr Thr Ser Ser Ala Glu Ser Arg Met Asp Phe Gln  
 370 375 380

<210> 65

<211> 1152

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1) .. (1152)

<223> 43301

<400> 65

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gcg gaa tgg gat tct cat gct caa act tgg atc ggt tgg cct gaa cgg 96  
 Ala Glu Trp Asp Ser His Ala Gln Thr Trp Ile Gly Trp Pro Glu Arg  
 20 25 30

caa gat aac tgg cgg cac aac gct tta ccc gca caa cga gtg ttt gca 144  
 Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala  
 35 40 45

gat gtt gca aag gcc atc tca aag ttc gag cct gtc act gtc tgt gct 192  
 Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala  
 50 55 60

agc cct gct cag tgg gaa aat gca agg aaa cag ctt cca gag gat ata 240  
 Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile  
 65 70 75 80

aga gtt gtt gag atg agc atg aat gat tct tgg ttc cgc gac tct gga 288  
 Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly  
 85 90 95

cca act ttc att gta cgg aaa aga cca gta aag ctc agt tct ctt aac 336

Pro	Thr	Phe	Ile	Val	Arg	Lys	Arg	Pro	Val	Lys	Leu	Ser	Ser	Leu	Asn	
			100					105					110			
cga	aac	att	gct	ggg	atc	gac	tgg	aat	ttc	aat	gcc	tgg	gga	gga	gct	384
Arg	Asn	Ile	Ala	Gly	Ile	Asp	Trp	Asn	Phe	Asn	Ala	Trp	Gly	Gly	Ala	
		115					120				125					
aat	gat	ggc	tgt	tac	aat	gat	tgg	agt	cat	gac	ctt	tta	gtt	tca	cga	432
Asn	Asp	Gly	Cys	Tyr	Asn	Asp	Trp	Ser	His	Asp	Leu	Leu	Val	Ser	Arg	
	130					135					140					
aag	att	ctc	gct	ttg	gaa	cga	att	cca	aga	ttt	caa	cat	tcg	atg	att	480
Lys	Ile	Leu	Ala	Leu	Glu	Arg	Ile	Pro	Arg	Phe	Gln	His	Ser	Met	Ile	
145					150					155					160	
ctt	gaa	gga	ggc	agc	atc	cat	gtc	gat	ggg	gaa	gga	acc	tgc	ctt	gtc	528
Leu	Glu	Gly	Gly	Ser	Ile	His	Val	Asp	Gly	Glu	Gly	Thr	Cys	Leu	Val	
				165					170					175		
aca	gaa	gag	tgt	ctc	ttg	aac	aaa	aac	cga	aac	cct	cat	atg	agt	aaa	576
Thr	Glu	Glu	Cys	Leu	Leu	Asn	Lys	Asn	Arg	Asn	Pro	His	Met	Ser	Lys	
			180					185					190			
gag	caa	ata	gag	gaa	gaa	ctt	aag	aag	tac	ctc	gga	gta	caa	tca	ttt	624
Glu	Gln	Ile	Glu	Glu	Glu	Leu	Lys	Lys	Tyr	Leu	Gly	Val	Gln	Ser	Phe	
		195					200					205				
atc	tgg	ctt	cct	cgt	ggc	ctt	tac	ggg	gat	gag	gac	aca	aat	ggc	cac	672
Ile	Trp	Leu	Pro	Arg	Gly	Leu	Tyr	Gly	Asp	Glu	Asp	Thr	Asn	Gly	His	
	210					215					220					
att	gat	aac	atg	tgc	tgc	ttc	gct	aga	ccg	gga	gtt	gtg	tta	ttg	tct	720
Ile	Asp	Asn	Met	Cys	Cys	Phe	Ala	Arg	Pro	Gly	Val	Val	Leu	Leu	Ser	
225					230					235					240	
tgg	aca	gac	gat	gaa	acc	gat	cct	caa	tac	gaa	agg	tct	gtg	gaa	gct	768
Trp	Thr	Asp	Asp	Glu	Thr	Asp	Pro	Gln	Tyr	Glu	Arg	Ser	Val	Glu	Ala	
				245					250					255		
ctt	tcg	gtt	ttg	tcg	aat	tcg	att	gat	gct	cgt	gga	agg	aag	att	caa	816
Leu	Ser	Val	Leu	Ser	Asn	Ser	Ile	Asp	Ala	Arg	Gly	Arg	Lys	Ile	Gln	
			260					265					270			
gtc	att	aaa	ctt	tat	atc	ccg	gaa	ccc	ctt	tat	atg	act	gaa	gaa	gaa	864
Val	Ile	Lys	Leu	Tyr	Ile	Pro	Glu	Pro	Leu	Tyr	Met	Thr	Glu	Glu	Glu	
		275					280					285				
tcg	tct	gga	atc	act	cag	gat	ggc	gaa	gct	ata	cca	aga	ctt	gca	ggg	912
Ser	Ser	Gly	Ile	Thr	Gln	Asp	Gly	Glu	Ala	Ile	Pro	Arg	Leu	Ala	Gly	
		290				295					300					
aca	aga	ctc	gca	gca	tcg	tat	gtg	aat	ttc	tac	atc	gcc	aat	gga	gga	960
Thr	Arg	Leu	Ala	Ala	Ser	Tyr	Val	Asn	Phe	Tyr	Ile	Ala	Asn	Gly	Gly	
305					310				315					320		
ata	atc	gct	cca	caa	ttc	ggc	gat	cca	ata	cgt	gat	aaa	gaa	gcg	att	1008
Ile	Ile	Ala	Pro	Gln	Phe	Gly	Asp	Pro	Ile	Arg	Asp	Lys	Glu	Ala	Ile	
				325					330					335		
cgt	gtc	ctc	tcg	gat	aca	ttt	cct	cat	cac	tcg	gtt	gtg	gga	atc	gag	1056

Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu  
 340 345 350  
 aat gca aga gag atc gtt ctt gct gga gga aac att cat tgt ata acg 1104  
 Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr  
 355 360 365  
 cag cag cag ccg gcg gag cct act tcc gtc gcc gaa aat ggc cac tga 1152  
 Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His  
 370 375 380

<210> 66

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 66

Met Glu Glu Ser Arg Glu Ser Pro Ala Glu His Gly Tyr Tyr Met Pro  
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 Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala  
 35 40 45  
 Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala  
 50 55 60  
 Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile  
 65 70 75 80  
 Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly  
 85 90 95  
 Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn  
 100 105 110  
 Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala  
 115 120 125  
 Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg  
 130 135 140

Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile  
 145 150 155 160  
 Leu Glu Gly Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val  
 165 170 175  
 Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys  
 180 185 190  
 Glu Gln Ile Glu Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe  
 195 200 205  
 Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His  
 210 215 220  
 Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser  
 225 230 235 240  
 Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala  
 245 250 255  
 Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln  
 260 265 270  
 Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu  
 275 280 285  
 Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly  
 290 295 300  
 Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly  
 305 310 315 320  
 Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile  
 325 330 335  
 Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu  
 340 345 350  
 Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr  
 355 360 365  
 Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His  
 370 375 380

&lt;210&gt; 67

&lt;211&gt; 1935

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1935)

&lt;223&gt; 46250

&lt;400&gt; 67

atg gct agt ctt ctt cga tcc tta atc ctt ttg cta atc gtg caa tca	48
Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Leu Ile Val Gln Ser	
1 5 10 15	
ttt ttg gtt gcg atc gct ttc ggg tcg aaa gaa gtt gaa gaa ttc agc	96
Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser	
20 25 30	
gag gca ttg ctc ttg aag cct tta cct gat cga aaa gtt tta gct cac	144
Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His	
35 40 45	
ttc cac ttc gag aac cga gct cct ccg tca aac tcc cat ggc cgc cat	192
Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His	
50 55 60	
cac cat ctc ttc ccg aaa gct att tct cag ttg gtt cag aag ttt cgg	240
His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg	
65 70 75 80	
gtc aag gag atg gag tta tct ttt act cag ggt cga tgg aac cat gaa	288
Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu	
85 90 95	
cat tgg gga gga ttt gac cct cta tca agt atg aat gcg aag cct gtt	336
His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val	
100 105 110	
ggg gtg gag ctg tgg gct gtg ttt gat gtt cct cag tct cag gtt gat	384
Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp	
115 120 125	
act tct tgg aag aac tta act cat gca ctg tca ggg ctt ttc tgt gct	432
Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala	
130 135 140	
tcc atc aat ttt cta gaa tct tcc act tca tat gct gct cct aca tgg	480
Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp	
145 150 155 160	

gga ttt gga ccc aat tct gac aag ctg agg tat ggt tca ctg cca cgt Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg 165 170 175	528
gaa gct gtt tgt act gag aac ttg acc cca tgg cta aag tta ctt cct Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro 180 185 190	576
tgt aga gat aag gat ggt att tct gcg tta atg aat agg cca tct gtt Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val 195 200 205	624
tac aga ggg ttt tat cat tct cag aga ttg cat tta tcc acg gtt gaa Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu 210 215 220	672
tct ggt caa gag gga ttg ggt tct ggt ata gtg ctg gag cag acg ctt Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu 225 230 235 240	720
act gtt gtt ctt cag cct gag act act tct gtt gaa tca aat atg cag Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln 245 250 255	768
cca agt tgg tcc ctc agc tcc ctc ttt ggg aga caa gtt gtt ggg aga Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg 260 265 270	816
tgt gtt ctt gca aag tca agt aat gtg tat ctt caa ttg gaa ggt ctt Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu 275 280 285	864
ctt ggt tac gaa tca aaa aac gtg gat aca gaa ata gaa gca cac caa Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln 290 295 300	912
cta tgg aag aat gca gag ttt gaa ttg tct ctt aag cca gag agg gtt Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val 305 310 315 320	960
att cga gaa agc tgc agc ttt ctt ttt att ttt gat att gac aaa tca Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser 325 330 335	1008
agt gac agc gag cca ttt gat ctt ggc ctt act tgg aag cgt ccc tca Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser 340 345 350	1056
aag tgg tca tgt caa caa gct cca tta cac tcg agt cgg ttt ttg atg Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met 355 360 365	1104
gga agc ggg aac gaa aga ggt gca ata gcc atc ttg tta aaa gcg aca Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr 370 375 380	1152
gaa tct cag gag aag tta tca ggc aga gat ctc act aat ggc caa tgt Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys 385 390 395 400	1200

aca ata aaa gca aat atc ttc cag att ttc cca tgg tat att aag gtt	1248
Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val	
405 410 415	
tat tat cat act cta caa atc ttt gtg gat caa caa cag aag aca gac	1296
Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp	
420 425 430	
agt gag gtc tta aag aag atc aat gtc tca cca tct acg gat aag gtg	1344
Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val	
435 440 445	
tca tct ggc atg atg gag atg atg ttg gaa cta cca tgt gaa gtg aaa	1392
Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys	
450 455 460	
tct gta gcc ata tca att gaa tat gat aag ggt ttt ctg cat ata gat	1440
Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp	
465 470 475 480	
gaa tat cct cct gat gct aat caa gga ttc gac att cca tcg gct ttg	1488
Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu	
485 490 495	
ata agc ttc ccc gat cat cat gct agt tta gat ttc caa gaa gag ctc	1536
Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu	
500 505 510	
agc aac tcg ccc tta tta tca agt tta aag gaa aaa tcc tta gta cgc	1584
Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg	
515 520 525	
tct tac aca gaa gta ttg ctc gta cct ttg aca acc cct gat ttt agc	1632
Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser	
530 535 540	
atg cct tac aac gta atc acg atc aca tgc acc atc ttc gca ttg tat	1680
Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr	
545 550 555 560	
ttt gga tca ttg cta aat gtt cta cgt aga cga att ggt gaa gaa gaa	1728
Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu	
565 570 575	
agg ttt ctc aaa agc caa gca gga aag aaa aca ggt ggg ctt aag cag	1776
Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln	
580 585 590	
tta tta tcg aga atc aca gcc aag att aga ggg aga cca att gaa gca	1824
Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala	
595 600 605	
cca tca tca tca gaa gct gaa tct tcg gtc ttg tct agt aaa ctt atc	1872
Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile	
610 615 620	
tta aaa atc ata tta gtt gca gga gct gct gca gcg tgg caa tat ttt	1920
Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Trp Gln Tyr Phe	
625 630 635 640	



tcc acg gac gag tag  
Ser Thr Asp Glu

1935

&lt;210&gt; 68

&lt;211&gt; 644

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 68

Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Leu Ile Val Gln Ser  
1 5 10 15

Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser  
20 25 30

Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His  
35 40 45

Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His  
50 55 60

His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg  
65 70 75 80

Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu  
85 90 95

His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val  
100 105 110

Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp  
115 120 125

Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala  
130 135 140

Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp  
145 150 155 160

Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg  
165 170 175

Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro  
 180 185 190

Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val  
 195 200 205

Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu  
 210 215 220

Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu  
 225 230 235 240

Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln  
 245 250 255

Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg  
 260 265 270

Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu  
 275 280 285

Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln  
 290 295 300

Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val  
 305 310 315 320

Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser  
 325 330 335

Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser  
 340 345 350

Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met  
 355 360 365

Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr  
 370 375 380

Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys  
 385 390 395 400

Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val  
 405 410 415

Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp  
 420 425 430

Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val  
 435 440 445

Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys  
 450 455 460

Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp  
 465 470 475 480

Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu  
 485 490 495

Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu  
 500 505 510

Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg  
 515 520 525

Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser  
 530 535 540

Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr  
 545 550 555 560

Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu  
 565 570 575

Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln  
 580 585 590

Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala  
 595 600 605

Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile  
 610 615 620

Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Ala Trp Gln Tyr Phe  
 625 630 635 640

Ser Thr Asp Glu

&lt;210&gt; 69

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (210)

&lt;223&gt; 47050A

&lt;400&gt; 69

atg ggt gga gga gga cat ggc gga ggt ata act tac aag gga gtc act	48
Met Gly Gly Gly Gly His Gly Gly Gly Ile Thr Tyr Lys Gly Val Thr	
1 5 10 15	

gtc cac act ccc aag act tgg cac acc gtc acc gga aaa ggc ttg tgc	96
Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys	
20 25 30	

gcc gtt atg tgg ttc tgg att ctg tac agg gca aag caa gat ggt cct	144
Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro	
35 40 45	

gta gtt atg gga tgg agg cac cct tgg gat ggt cat ggt gat cac ggt	192
Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly	
50 55 60	

cac gga gat cat cac tag	210
His Gly Asp His His	
65	

&lt;210&gt; 70

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 70

Met Gly Gly Gly Gly His Gly Gly Gly Ile Thr Tyr Lys Gly Val Thr
1 5 10 15

Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys  
                   20                                  25                                  30

Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro  
                   35                                  40                                  45

Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly  
           50                                  55                                  60

His Gly Asp His His  
   65

<210> 71

<211> 978

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(978)

<223> 52949A

<400> 71  
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 Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro  
 1                                  5                                  10                                  15

act aac ctt cgt tca aat cac cat ctc ccc act ttc ttc ccc aag aat 96  
 Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn  
                   20                                  25                                  30

tat ctc att tgc tct cat tcc act tct tct cgc ttc gaa tcg ctc tcg 144  
 Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser  
                   35                                  40                                  45

gtt tca tcg atc gga act gga tct acc aag aaa tca tcc gat act cgg 192  
 Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg  
                   50                                  55                                  60

aga aag gta aag agc atg gct acg aca aat ata gga aag gag gag aag 240  
 Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys  
 65                                  70                                  75                                  80

aaa aga gtc gag att tat gat ctc gaa gag aat tta gtg att gat ttg 288  
 Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu  
                   85                                  90                                  95

gct aaa ttc aca gca gat ctc tcc gat aag ttt tgt aaa gag aga ggc	336
Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly	
100 105 110	
gct ttc acc gtc gtt gtc tcc ggt ggc tct ctc atc aaa tca ctc cgg	384
Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg	
115 120 125	
aaa tta gta gaa tct cct tac gtt gat tct ata gat tgg gca agg tgg	432
Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp	
130 135 140	
cat ttt ttc tgg gtt gac gag aga gtt gtt ccc aag aat cac gat gat	480
His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp	
145 150 155 160	
agc aac tat aaa ctc gct tat gat agt ttt cta tcc aag gta cca att	528
Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile	
165 170 175	
ccg cct gga aat gta tat gca atc aac gaa gcc ctc tcc gct gag gct	576
Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala	
180 185 190	
gca gcg gat gat tac gag acc tgc ctc aaa cat ttg gtc aac acc aac	624
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn	
195 200 205	
att ctc cgt gta tct gaa tca act ggc ttt ccc aaa ttt gat ctc atg	672
Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met	
210 215 220	
ctt cta ggt atg gga cct gat ggt cat gtg gca tca tta ttc cct ggg	720
Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly	
225 230 235 240	
cat ggt ctc tgc aac gag agc aag aaa tgg gta gtt tca atc tct gac	768
His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp	
245 250 255	
tct cca aaa cca ccg tct gag aga atc acc ttc acg ttc ccg gtc atc	816
Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile	
260 265 270	
aac tca tct gca cat gta gct cta gtt gtt tgc ggt tct ggg aaa gct	864
Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala	
275 280 285	
gaa gct gtg gag gca gct tta aag aag act ggg aat gta cca cct gct	912
Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala	
290 295 300	
ggt tct gtt tct gct gaa gac gag ttg gtt tgg ttc ctg gac aaa cca	960
Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro	
305 310 315 320	
gca tct tcc aag ctc taa	978
Ala Ser Ser Lys Leu	
325	

&lt;210&gt; 72

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 72

Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro  
 1 5 10 15

Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn  
 20 25 30

Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser  
 35 40 45

Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg  
 50 55 60

Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys  
 65 70 75 80

Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu  
 85 90 95

Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly  
 100 105 110

Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg  
 115 120 125

Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp  
 130 135 140

His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp  
 145 150 155 160

Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile  
 165 170 175

Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala  
 180 185 190

Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn  
 195 200 205

Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met  
 210 215 220

Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly  
 225 230 235 240

His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp  
 245 250 255

Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile  
 260 265 270

Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala  
 275 280 285

Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala  
 290 295 300

Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro  
 305 310 315 320

Ala Ser Ser Lys Leu  
 325

<210> 73

<211> 2343

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (2343)

<223> 53210A

<400> 73

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48



Met	Ala	Pro	Ala	Leu	Ser	Arg	Ser	Leu	Tyr	Thr	Ser	Pro	Leu	Thr	Ser	
1				5					10					15		
ggt	cca	atc	act	cct	gtc	tct	tct	cgt	ctc	tct	cat	ctg	aga	agc	tcg	96
Val	Pro	Ile	Thr	Pro	Val	Ser	Ser	Arg	Leu	Ser	His	Leu	Arg	Ser	Ser	
			20					25					30			
ttt	ctc	cca	cac	ggc	ggc	gct	tta	aga	acc	ggc	gtt	tcg	tgt	agc	tgg	144
Phe	Leu	Pro	His	Gly	Gly	Ala	Leu	Arg	Thr	Gly	Val	Ser	Cys	Ser	Trp	
		35					40					45				
aat	ctc	gaa	aag	aga	tgt	aac	cga	ttc	gcc	gtg	aag	tgt	gac	gcc	gcc	192
Asn	Leu	Glu	Lys	Arg	Cys	Asn	Arg	Phe	Ala	Val	Lys	Cys	Asp	Ala	Ala	
		50				55					60					
gtg	gcg	gag	aaa	gag	acc	act	gaa	gaa	ggg	tca	ggt	gag	aag	ttt	gag	240
Val	Ala	Glu	Lys	Glu	Thr	Thr	Glu	Glu	Gly	Ser	Gly	Glu	Lys	Phe	Glu	
65					70				75					80		
tac	caa	gct	gag	gtt	agt	aga	ttg	ttg	gat	ttg	att	gtt	cat	agc	tta	288
Tyr	Gln	Ala	Glu	Val	Ser	Arg	Leu	Leu	Asp	Leu	Ile	Val	His	Ser	Leu	
			85						90					95		
tac	agt	cac	aag	gag	gtg	ttt	ctc	agg	gag	ctt	gta	agt	aat	gca	agt	336
Tyr	Ser	His	Lys	Glu	Val	Phe	Leu	Arg	Glu	Leu	Val	Ser	Asn	Ala	Ser	
			100					105					110			
gat	gct	ttg	gat	aag	ctg	agg	ttc	ttg	agt	gta	aca	gag	cct	tct	ttg	384
Asp	Ala	Leu	Asp	Lys	Leu	Arg	Phe	Leu	Ser	Val	Thr	Glu	Pro	Ser	Leu	
			115				120					125				
ctt	gga	gat	ggt	gga	gat	ctt	gag	att	agg	att	aag	cct	gat	cct	gat	432
Leu	Gly	Asp	Gly	Gly	Asp	Leu	Glu	Ile	Arg	Ile	Lys	Pro	Asp	Pro	Asp	
		130				135					140					
aac	ggc	acc	atc	acc	ata	act	gat	act	ggt	att	gga	atg	aca	aag	gaa	480
Asn	Gly	Thr	Ile	Thr	Ile	Thr	Asp	Thr	Gly	Ile	Gly	Met	Thr	Lys	Glu	
145					150					155					160	
gaa	ctt	att	gat	tgc	ctt	gga	act	att	gct	caa	agt	ggt	act	tcg	aaa	528
Glu	Leu	Ile	Asp	Cys	Leu	Gly	Thr	Ile	Ala	Gln	Ser	Gly	Thr	Ser	Lys	
				165					170					175		
ttc	ttg	aag	gct	cta	aag	gaa	aac	aag	gac	ctt	ggt	gct	gac	aac	ggt	576
Phe	Leu	Lys	Ala	Leu	Lys	Glu	Asn	Lys	Asp	Leu	Gly	Ala	Asp	Asn	Gly	
			180					185					190			
ttg	atc	gga	cag	ttt	ggt	gtt	ggg	ttt	tac	tct	gct	ttc	tta	gtt	gct	624
Leu	Ile	Gly	Gln	Phe	Gly	Val	Gly	Phe	Tyr	Ser	Ala	Phe	Leu	Val	Ala	
		195					200					205				
gag	aag	gtt	gtt	gtg	tcc	acc	aaa	agc	ccc	aaa	tct	gac	aag	caa	tat	672
Glu	Lys	Val	Val	Val	Ser	Thr	Lys	Ser	Pro	Lys	Ser	Asp	Lys	Gln	Tyr	
		210				215					220					
gtt	tgg	gaa	tcg	gtt	gcc	gat	agt	agc	tcg	tat	ctg	atc	aga	gaa	gaa	720
Val	Trp	Glu	Ser	Val	Ala	Asp	Ser	Ser	Ser	Tyr	Leu	Ile	Arg	Glu	Glu	
225					230					235					240	
aca	gac	cct	gat	aac	att	cta	cgt	cgt	gga	aca	caa	atc	acc	ttg	tat	768

Thr	Asp	Pro	Asp	Asn	Ile	Leu	Arg	Arg	Gly	Thr	Gln	Ile	Thr	Leu	Tyr	
				245					250					255		
ctg	agg	gag	gat	gat	aaa	tac	gaa	ttt	gcg	gag	tct	aca	agg	atc	aag	816
Leu	Arg	Glu	Asp	Asp	Lys	Tyr	Glu	Phe	Ala	Glu	Ser	Thr	Arg	Ile	Lys	
			260					265					270			
aac	ctc	gtg	aag	aat	tac	tct	cag	ttc	gtt	ggg	ttt	cct	atc	tat	aca	864
Asn	Leu	Val	Lys	Asn	Tyr	Ser	Gln	Phe	Val	Gly	Phe	Pro	Ile	Tyr	Thr	
		275					280					285				
tgg	cag	gag	aaa	tca	agg	act	ata	gag	gtc	gaa	gag	gac	gaa	cca	gtt	912
Trp	Gln	Glu	Lys	Ser	Arg	Thr	Ile	Glu	Val	Glu	Glu	Asp	Glu	Pro	Val	
	290					295					300					
aag	gaa	gga	gaa	gag	ggt	gag	cca	aag	aaa	aag	aag	acc	act	aaa	act	960
Lys	Glu	Gly	Glu	Glu	Gly	Glu	Pro	Lys	Lys	Lys	Lys	Thr	Thr	Lys	Thr	
305					310					315					320	
gag	aag	tat	tgg	gat	tgg	gaa	cta	gcc	aac	gag	acc	aaa	ccg	cta	tgg	1008
Glu	Lys	Tyr	Trp	Asp	Trp	Glu	Leu	Ala	Asn	Glu	Thr	Lys	Pro	Leu	Trp	
				325					330					335		
atg	cgc	aat	tcg	aag	gaa	gtg	gaa	aaa	gga	gag	tac	aat	gag	ttc	tac	1056
Met	Arg	Asn	Ser	Lys	Glu	Val	Glu	Lys	Gly	Glu	Tyr	Asn	Glu	Phe	Tyr	
			340					345					350			
aaa	aag	gct	ttc	aat	gag	ttc	ttg	gat	cca	ctt	gct	cac	aca	cac	ttc	1104
Lys	Lys	Ala	Phe	Asn	Glu	Phe	Leu	Asp	Pro	Leu	Ala	His	Thr	His	Phe	
		355					360					365				
aca	act	gag	ggt	gag	gtt	gag	ttc	agg	agc	att	ttg	tac	atc	cct	ggg	1152
Thr	Thr	Glu	Gly	Glu	Val	Glu	Phe	Arg	Ser	Ile	Leu	Tyr	Ile	Pro	Gly	
		370				375					380					
atg	ggt	cct	ctt	aac	aat	gaa	gat	gtt	aca	aac	ccg	aaa	aca	aag	aac	1200
Met	Gly	Pro	Leu	Asn	Asn	Glu	Asp	Val	Thr	Asn	Pro	Lys	Thr	Lys	Asn	
385					390					395					400	
att	cgt	ctc	tac	gtg	aag	cgt	gtg	ttt	atc	tct	gac	gat	ttt	gat	gga	1248
Ile	Arg	Leu	Tyr	Val	Lys	Arg	Val	Phe	Ile	Ser	Asp	Asp	Phe	Asp	Gly	
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gag	ctt	ttc	ccg	aga	tat	ctg	agc	ttt	gtg	aag	gga	gtt	gtg	gac	tct	1296
Glu	Leu	Phe	Pro	Arg	Tyr	Leu	Ser	Phe	Val	Lys	Gly	Val	Val	Asp	Ser	
			420					425					430			
gat	gat	ctt	cct	ctt	aat	gtt	tct	cgt	gaa	att	ctc	caa	gaa	agc	aga	1344
Asp	Asp	Leu	Pro	Leu	Asn	Val	Ser	Arg	Glu	Ile	Leu	Gln	Glu	Ser	Arg	
			435				440					445				
att	gta	aga	atc	atg	aga	aag	agg	ctc	att	aga	aaa	acc	ttt	gac	atg	1392
Ile	Val	Arg	Ile	Met	Arg	Lys	Arg	Leu	Ile	Arg	Lys	Thr	Phe	Asp	Met	
		450				455					460					
ata	caa	gaa	atc	tct	gag	agt	gaa	aac	aaa	gag	gat	tac	aag	aaa	ttc	1440
Ile	Gln	Glu	Ile	Ser	Glu	Ser	Glu	Asn	Lys	Glu	Asp	Tyr	Lys	Lys	Phe	
465					470					475					480	
tgg	gag	aac	ttt	ggt	aga	ttc	ctt	aaa	ttg	ggt	tgt	att	gaa	gac	acc	1488

Trp	Glu	Asn	Phe	Gly	Arg	Phe	Leu	Lys	Leu	Gly	Cys	Ile	Glu	Asp	Thr		
				485					490					495			
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Gly	Asn	His	Lys	Arg	Ile	Thr	Pro	Leu	Leu	Arg	Phe	Phe	Ser	Ser	Lys		
			500					505					510				
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Asn	Glu	Glu	Glu	Leu	Thr	Ser	Leu	Asp	Asp	Tyr	Ile	Glu	Asn	Met	Gly		
			515					520				525					
gag	aac	caa	aag	gcg	atc	tac	tac	ctc	gca	act	gat	agt	ctt	aaa	agt	1632	
Glu	Asn	Gln	Lys	Ala	Ile	Tyr	Tyr	Leu	Ala	Thr	Asp	Ser	Leu	Lys	Ser		
			530				535				540						
gcc	aag	tct	gcc	cct	ttc	ttg	gag	aaa	cta	atc	caa	aaa	gat	atc	gag	1680	
Ala	Lys	Ser	Ala	Pro	Phe	Leu	Glu	Lys	Leu	Ile	Gln	Lys	Asp	Ile	Glu		
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gtt	cta	tat	ttg	gtt	gaa	cca	atc	gat	gaa	gtt	gct	att	cag	aat	ttg	1728	
Val	Leu	Tyr	Leu	Val	Glu	Pro	Ile	Asp	Glu	Val	Ala	Ile	Gln	Asn	Leu		
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caa	acc	tac	aaa	gaa	aag	aaa	ttc	gtt	gat	atc	agt	aaa	gaa	gat	ttg	1776	
Gln	Thr	Tyr	Lys	Glu	Lys	Lys	Phe	Val	Asp	Ile	Ser	Lys	Glu	Asp	Leu		
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gaa	ctc	gga	gat	gaa	gat	gaa	gta	aag	gac	agg	gaa	gcg	aaa	caa	gag	1824	
Glu	Leu	Gly	Asp	Glu	Asp	Glu	Val	Lys	Asp	Arg	Glu	Ala	Lys	Gln	Glu		
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ttt	aac	ctt	ctc	tgt	gac	tgg	ata	aaa	cag	cag	ctc	ggt	gac	aaa	gtt	1872	
Phe	Asn	Leu	Leu	Cys	Asp	Trp	Ile	Lys	Gln	Gln	Leu	Gly	Asp	Lys	Val		
			610				615				620						
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Ala	Lys	Val	Gln	Val	Ser	Asn	Arg	Leu	Ser	Ser	Ser	Pro	Cys	Val	Leu		
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gtc	tct	ggc	aaa	ttc	ggg	tgg	tca	gct	aat	atg	gaa	agg	cta	atg	aag	1968	
Val	Ser	Gly	Lys	Phe	Gly	Trp	Ser	Ala	Asn	Met	Glu	Arg	Leu	Met	Lys		
				645					650					655			
gca	cag	gct	ctt	gga	gac	act	tca	agc	ctg	gag	ttc	atg	aga	ggt	agg	2016	
Ala	Gln	Ala	Leu	Gly	Asp	Thr	Ser	Ser	Leu	Glu	Phe	Met	Arg	Gly	Arg		
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aga	ata	cta	gag	atc	aat	cca	gat	cat	ccc	atc	atc	aaa	gac	ttg	aac	2064	
Arg	Ile	Leu	Glu	Ile	Asn	Pro	Asp	His	Pro	Ile	Ile	Lys	Asp	Leu	Asn		
			675				680					685					
gct	gct	tgt	aag	aat	gca	cca	gag	agc	act	gaa	gca	aca	aga	gtg	gtc	2112	
Ala	Ala	Cys	Lys	Asn	Ala	Pro	Glu	Ser	Thr	Glu	Ala	Thr	Arg	Val	Val		
			690			695					700						
gat	ctc	ttg	tat	gac	act	gct	ata	ata	tca	agt	gga	ttc	act	cct	gat	2160	
Asp	Leu	Leu	Tyr	Asp	Thr	Ala	Ile	Ile	Ser	Ser	Gly	Phe	Thr	Pro	Asp		
					710					715					720		
agc	ccg	gcc	gag	ctc	ggg	aac	aag	ata	tat	gag	atg	atg	gca	atg	gcg	2208	

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Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp  
35 40 45

Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala  
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Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu  
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Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu  
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Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser  
100 105 110

Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu  
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Leu Gly Asp Gly Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp  
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Asn Gly Thr Ile Thr Ile Thr Asp Thr Gly Ile Gly Met Thr Lys Glu  
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Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys  
 165 170 175

Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly  
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Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala  
 195 200 205

Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr  
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Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu  
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Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr  
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Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys  
 260 265 270

Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr  
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Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Glu Asp Glu Pro Val  
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Lys Glu Gly Glu Glu Gly Glu Pro Lys Lys Lys Lys Thr Thr Lys Thr  
 305 310 315 320

Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp  
 325 330 335

Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr  
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Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe  
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Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly  
 370 375 380

Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn  
 385 390 395 400

Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly  
 405 410 415

Glu Leu Phe Pro Arg Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser  
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Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg  
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Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met  
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Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe  
 465 470 475 480

Trp Glu Asn Phe Gly Arg Phe Leu Lys Leu Gly Cys Ile Glu Asp Thr  
 485 490 495

Gly Asn His Lys Arg Ile Thr Pro Leu Leu Arg Phe Phe Ser Ser Lys  
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Asn Glu Glu Glu Leu Thr Ser Leu Asp Asp Tyr Ile Glu Asn Met Gly  
 515 520 525

Glu Asn Gln Lys Ala Ile Tyr Tyr Leu Ala Thr Asp Ser Leu Lys Ser  
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Val Leu Tyr Leu Val Glu Pro Ile Asp Glu Val Ala Ile Gln Asn Leu  
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Gln Thr Tyr Lys Glu Lys Lys Phe Val Asp Ile Ser Lys Glu Asp Leu  
 580 585 590

Glu Leu Gly Asp Glu Asp Glu Val Lys Asp Arg Glu Ala Lys Gln Glu  
 595 600 605

Phe Asn Leu Leu Cys Asp Trp Ile Lys Gln Gln Leu Gly Asp Lys Val  
 610 615 620

Ala Lys Val Gln Val Ser Asn Arg Leu Ser Ser Ser Pro Cys Val Leu  
 625 630 635 640

Val Ser Gly Lys Phe Gly Trp Ser Ala Asn Met Glu Arg Leu Met Lys  
 645 650 655

Ala Gln Ala Leu Gly Asp Thr Ser Ser Leu Glu Phe Met Arg Gly Arg  
 660 665 670

Arg Ile Leu Glu Ile Asn Pro Asp His Pro Ile Ile Lys Asp Leu Asn  
 675 680 685

Ala Ala Cys Lys Asn Ala Pro Glu Ser Thr Glu Ala Thr Arg Val Val  
 690 695 700

Asp Leu Leu Tyr Asp Thr Ala Ile Ile Ser Ser Gly Phe Thr Pro Asp  
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Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala  
 725 730 735

Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Glu Ser Ser Thr  
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Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser	
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cct aaa tgg aag aaa agt ttc att agt tta cct tgt cgt agt aaa act	144
Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr	
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acg agg aag gtt ttg gcg tca agc cgt tat gtg cca ggg aaa ttg gaa	192
Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu	
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Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu	
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aag ctt ggt ttt gtg agg act ttg ttg att gat aat tat gat agt tat	288
Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr	
85 90 95	
aca ttc aat ata tat cag gct ctg agt act att aat gga gtg cct cct	336
Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro	
100 105 110	
gtc gtt att cgg aat gat gag tgg acg tgg gaa gaa gct tac cat tac	384
Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr	
115 120 125	
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Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro	
130 135 140	
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Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu	
145 150 155 160	
ctt gaa tgc cgt gat atc cca att cta ggc gtc tgc ctt ggc cac cag	528
Leu Glu Cys Arg Asp Ile Pro Ile Leu Gly Val Cys Leu Gly His Gln	
165 170 175	
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Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro	
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gtc cat gga cgg ttg agt ggg att gaa cat gat ggg aac ata ttg ttt	624
Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe	
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Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr	
210 215 220	



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cat tct tct ttt ccc cat tat ggt tta cag ttt cat cca gaa agt att His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile 305 310 315 320	960
gct act acc tat ggt agt cag tta ttt aaa aat ttc aag gac ata act Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr 325 330 335	1008
gtg aat tat tgg agt cgg tgc aaa tct aca tcc ctg cgt cga aga aac Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Arg Asn 340 345 350	1056
ata aat gac act gca aac atg cag gtg cct gat gct act caa ttg ctg Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu 355 360 365	1104
aaa gaa ctt tct aga act aga tgt aca gga aat ggt tct agc tat ttt Lys Glu Leu Ser Arg Thr Arg Cys Thr Gly Asn Gly Ser Ser Tyr Phe 370 375 380	1152
ggg aac cct aag tct ctg ttt tct gcc aag aca aat ggt gta gac gtc Gly Asn Pro Lys Ser Leu Phe Ser Ala Lys Thr Asn Gly Val Asp Val 385 390 395 400	1200
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agg ttg aaa tgg aag aag cat gaa cgt ctt gcg cat aaa gtt ggt gga Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly 420 425 430	1296
gta aga aat ata ttt atg gaa ctc ttt ggc aag aat aga gga aat gat Val Arg Asn Ile Phe Met Glu Leu Phe Gly Lys Asn Arg Gly Asn Asp 435 440 445	1344
act ttt tgg ctg gat act tct tct agt gac aag gct aga gga cga ttt Thr Phe Trp Leu Asp Thr Ser Ser Ser Asp Lys Ala Arg Gly Arg Phe 450 455 460	1392

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Ser Phe Met Gly Gly Lys Gly Gly Ser Leu Trp Lys Gln Leu Thr Phe	
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agt tta tct gat caa agt gag gtt aca tca aaa cat gcg gga cat ctt	1488
Ser Leu Ser Asp Gln Ser Glu Val Thr Ser Lys His Ala Gly His Leu	
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Leu Ile Glu Asp Ser Gln Ser Ser Thr Glu Lys Gln Phe Leu Glu Glu	
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Gly Phe Leu Asp Phe Leu Arg Lys Glu Leu Ser Ser Ile Ser Tyr Asp	
515 520 525	
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Glu Lys Asp Phe Glu Glu Leu Pro Phe Asp Phe Cys Gly Gly Tyr Val	
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Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro	
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Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys	
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Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn	
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att gtg ata aga aca gta ata ata cat gaa gat gaa gct tcc att gga Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly 865 870 875 880	2640
gca gga gga gct att gtt gca tta tca agt cca gaa gat gag ttt gag Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu 885 890 895	2688
gaa atg att ctt aag act aga gct cct gct aat gca gtc atg gag ttt Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe 900 905 910	2736
tgt agt gat cag agg aga caa tag Cys Ser Asp Gln Arg Arg Gln 915	2760

&lt;211&gt; 919

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

Met Asn Met Asn Phe Ser Phe Cys Ser Thr Ser Ser Glu Leu Ser Tyr  
 1 5 10 15

Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser  
 20 25 30

Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr  
 35 40 45

Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu  
 50 55 60

Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu  
 65 70 75 80

Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr  
 85 90 95

Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro  
 100 105 110

Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr  
 115 120 125

Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro  
 130 135 140

Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu  
 145 150 155 160

Leu Glu Cys Arg Asp Ile Pro Ile Leu Gly Val Cys Leu Gly His Gln  
 165 170 175

Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro  
 180 185 190

Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe  
 195 200 205

Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr  
 210 215 220

His Ser Leu Ile Ile Asp Lys Glu Ser Leu Pro Lys Glu Leu Val Pro  
 225 230 235 240

Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn  
 245 250 255

Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser  
 260 265 270

Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser  
 275 280 285

Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met  
 290 295 300

His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile  
 305 310 315 320

Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr  
 325 330 335

Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Arg Asn  
 340 345 350

Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu  
 355 360 365

Lys Glu Leu Ser Arg Thr Arg Cys Thr Gly Asn Gly Ser Ser Tyr Phe  
 370 375 380

Gly Asn Pro Lys Ser Leu Phe Ser Ala Lys Thr Asn Gly Val Asp Val  
 385 390 395 400

Phe Asp Met Val Asp Ser Ser Tyr Pro Lys Pro His Thr Lys Leu Leu  
 405 410 415

Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly  
 420 425 430

Val Arg Asn Ile Phe Met Glu Leu Phe Gly Lys Asn Arg Gly Asn Asp  
 435 440 445

Thr Phe Trp Leu Asp Thr Ser Ser Ser Asp Lys Ala Arg Gly Arg Phe  
 450 455 460

Ser Phe Met Gly Gly Lys Gly Gly Ser Leu Trp Lys Gln Leu Thr Phe  
 465 470 475 480

Ser Leu Ser Asp Gln Ser Glu Val Thr Ser Lys His Ala Gly His Leu  
 485 490 495

Leu Ile Glu Asp Ser Gln Ser Ser Thr Glu Lys Gln Phe Leu Glu Glu  
 500 505 510

Gly Phe Leu Asp Phe Leu Arg Lys Glu Leu Ser Ser Ile Ser Tyr Asp  
 515 520 525

Glu Lys Asp Phe Glu Glu Leu Pro Phe Asp Phe Cys Gly Gly Tyr Val  
 530 535 540

Gly Cys Ile Gly Tyr Asp Ile Lys Val Glu Cys Gly Met Pro Ile Asn  
 545 550 555 560

Arg His Lys Ser Asn Ala Pro Asp Ala Cys Phe Phe Phe Ala Asp Asn  
 565 570 575

Val Val Ala Ile Asp His Gln Leu Asp Asp Val Tyr Ile Leu Ser Leu  
 580 585 590

Tyr Glu Glu Gly Thr Ala Glu Thr Ser Phe Leu Asn Asp Thr Glu Glu  
 595 600 605

Lys Leu Ile Ser Leu Met Gly Leu Ser Thr Arg Lys Leu Glu Asp Gln  
 610 615 620

Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro  
 625 630 635 640

Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys  
 645 650 655

Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn  
 660 665 670

Arg Arg Lys Ile Gly Asn Ala Asp Pro Leu Gly Leu Tyr Leu His Leu  
 675 680 685

Arg Glu Arg Asn Pro Ala Pro Tyr Ala Ala Phe Leu Asn Phe Ser Asn  
690 695 700

Ala Asn Leu Ser Leu Cys Ser Ser Ser Pro Glu Arg Phe Leu Lys Leu  
705 710 715 720

Asp Arg Asn Gly Met Leu Glu Ala Lys Pro Ile Lys Gly Thr Ile Ala  
725 730 735

Arg Gly Ser Thr Pro Glu Glu Asp Glu Phe Leu Lys Leu Gln Leu Lys  
740 745 750

Leu Ser Glu Lys Asn Gln Ala Glu Asn Leu Met Ile Val Asp Leu Leu  
755 760 765

Arg Asn Asp Leu Gly Arg Val Cys Glu Pro Gly Ser Val His Val Pro  
770 775 780

Asn Leu Met Asp Val Glu Ser Tyr Thr Thr Val His Thr Met Val Ser  
785 790 795 800

Thr Ile Arg Gly Leu Lys Lys Thr Asp Ile Ser Pro Val Glu Cys Val  
805 810 815

Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly Ala Pro Lys Leu Arg  
820 825 830

Ser Val Glu Ile Leu Asp Ser Leu Glu Asn Cys Ser Arg Gly Leu Tyr  
835 840 845

Ser Gly Ser Ile Gly Tyr Phe Ser Tyr Asn Gly Thr Phe Asp Leu Asn  
850 855 860

Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly  
865 870 875 880

Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu  
885 890 895

Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe  
900 905 910

Cys Ser Asp Gln Arg Arg Gln  
915

&lt;210&gt; 77

&lt;211&gt; 1329

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1329)

&lt;223&gt; 58351A

&lt;400&gt; 77

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Met Gly Asp Ser Gly Lys Leu Glu Ala Thr Ile Asp Arg Leu Leu Asn	
1 5 10 15	

gaa gag aag cag atg aga ctc gcc gaa aac gta gcc ggt aca agg aaa	96
Glu Glu Lys Gln Met Arg Leu Ala Glu Asn Val Ala Gly Thr Arg Lys	
20 25 30	

gcc gcc act gag att ctt cag ctt tgt ttc gat gct aag gat tgg aaa	144
Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys	
35 40 45	

ctt ctg aat gag cag att ctc aat ctc tct aag aaa cgt ggt cag ctc	192
Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu	
50 55 60	

aaa cag gct gtg caa tcc atg gtg cag caa gca atg cag tat atc gat	240
Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp	
65 70 75 80	

cag aca cca gac att gaa act cgg ata gag ctt atc aag acg ctg aac	288
Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn	
85 90 95	

aat gta tct gct gga aag ata tat gtt gaa atc gag agg gca cgt ctc	336
Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu	
100 105 110	

acc aag aaa ctt gct aag att aag gaa gaa cag ggt cag ata gct gaa	384
Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu	
115 120 125	

gct gca gat ctt atg caa gaa gtt gct gtg gag aca ttt ggt gct atg	432
Ala Ala Asp Leu Met Gln Val Ala Val Glu Thr Phe Gly Ala Met	
130 135 140	

gca aaa act gag aaa att gca ttt atc ctt gaa caa gtt cgc ttg tgc	480
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Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys	
145 150 155 160	
ttg gat cgt caa gat ttt gtt cgt gca caa atc tta tct agg aag atc	528
Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile	
165 170 175	
aat cct aga gtt ttt gac gca gat aca aaa aaa gat aag aag aaa cct	576
Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Lys Pro	
180 185 190	
aag gaa ggt gat aac atg gta gaa gag gct cct gct gat ata cca acc	624
Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr	
195 200 205	
ctt ttg gag ctt aag cga att tac tac gag ctt atg att cgg tac tat	672
Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr	
210 215 220	
tct cat aac aat gag tac att gaa atc tgc cgt agc tac aag gcg ata	720
Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile	
225 230 235 240	
tat gat atc cct tca gta aaa gaa act ccg gag cag tgg att ccg gtc	768
Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val	
245 250 255	
ctg agg aag atc tgc tgg ttc ttg gtc ttg gca cct cat gac cca atg	816
Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met	
260 265 270	
caa tca agc ttg ctc aat gca act ctg gaa gac aag aat tta tca gaa	864
Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu	
275 280 285	
atc cct gat ttc aag atg ctt cta aaa cag gta gtg aca atg gag gtt	912
Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val	
290 295 300	
att caa tgg aca tct ctg tgg aac aaa tac aag gat gag ttc gag aaa	960
Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys	
305 310 315 320	
gag aaa agc atg att gga ggt tct ttg ggt gac aaa gct ggt gaa gat	1008
Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp	
325 330 335	
ctg aaa ctg aga atc atc gaa cat aat atc ctc gtt gtc tca aag tac	1056
Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr	
340 345 350	
tac gca agg ata acc tta aag aga ctt gcc gag ctt tta tgc ctg agc	1104
Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser	
355 360 365	
atg gag gag gcg gag aag cat cta tcg gag atg gta gtg tca aaa gca	1152
Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala	
370 375 380	
ctg att gca aaa ata gac aga cca tct gga att gtg tgc ttc cag atc	1200

Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile  
 385 390 395 400  
 gca aag gac agc aac gag att cta aac tcg tgg gca ggg aat ttg gag 1248  
 Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu 415  
 405 410  
 aag ctt cta gat ctt gtg gaa aag agt tgc cac caa att cac aag gaa 1296  
 Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu 430  
 420 425  
 acc atg gtt cac aaa gcc gct ctc aga cct tga 1329  
 Thr Met Val His Lys Ala Ala Leu Arg Pro 440  
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<210> 78

<211> 442

<212> PRT

<213> Arabidopsis thaliana

<400> 78

Met Gly Asp Ser Gly Lys Leu Glu Ala Thr Ile Asp Arg Leu Leu Asn  
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 20 25 30  
 Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys  
 35 40 45  
 Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu  
 50 55 60  
 Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp  
 65 70 75 80  
 Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn  
 85 90 95  
 Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu  
 100 105 110  
 Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu  
 115 120 125

Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met  
 130 135 140

Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys  
 145 150 155 160

Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile  
 165 170 175

Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Lys Pro  
 180 185 190

Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr  
 195 200 205

Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr  
 210 215 220

Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile  
 225 230 235 240

Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val  
 245 250 255

Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met  
 260 265 270

Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu  
 275 280 285

Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val  
 290 295 300

Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys  
 305 310 315 320

Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp  
 325 330 335

Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr  
 340 345 350

Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser  
 355 360 365

Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala  
 370 375 380

Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile  
 385 390 395 400

Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu  
 405 410 415

Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu  
 420 425 430

Thr Met Val His Lys Ala Ala Leu Arg Pro  
 435 440

<210> 79

<211> 435

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(435)

<223> 60944

<400> 79

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 1 5 10 15

cct tct ctg caa tta aga aag ccg gtg atg gcg gca gtg aaa gga gga 96  
 Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly  
 20 25 30

aaa caa tcg gtg aga aga agc agc aat acg gtg gtt cag ata acg tgt 144  
 Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys  
 35 40 45

cgt aag aag gaa ttg cat cct gaa ttc cac gaa gac gca aag gtt tac 192  
 Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr  
 50 55 60

tgc aat gga gag ctg gtg atg act aca gga gga aca aag aaa gag tat 240  
 Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr  
 65 70 75 80

gtg gtt gat gta tgg tca ggt aac cat ccg ttt tac ctc ggg aat cgt 288  
Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg  
85 90 95

tcg gct ttg atg gtt gat gct gat caa gtt gag aag ttt cgt aag agg 336  
Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg  
100 105 110

ttc gct ggg ctt tct gag att atg gag att cct gtg ctt aaa gga gaa 384  
Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu  
115 120 125

atc att atg cct act aag aaa agt aaa ggt ccc aaa ggg aag aag aaa 432  
Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys  
130 135 140

tga 435

&lt;210&gt; 80

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 80

Met Ala Val Ser Leu Pro Asn Ser Phe Leu Gln Ile Ser Pro Cys Val  
1 5 10 15

Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly  
20 25 30

Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys  
35 40 45

Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr  
50 55 60

Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr  
65 70 75 80

Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg  
85 90 95

Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg  
100 105 110

Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu  
 115 120 125

Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys  
 130 135 140

<210> 81

<211> 2859

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (2859)

<223> 62837

<400> 81

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 Met Ala Trp Ser Ile Ala Leu Leu Thr Pro Pro Phe Phe Gly Pro Gly  
 1 5 10 15

agg cat gtg cag gcc aaa gaa tac agg gaa cca aga ggg tgt gtg atg 96  
 Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met  
 20 25 30

aag atg agc agt tta aaa gca cct gtt ctg aga att cag gcc aca gaa 144  
 Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu  
 35 40 45

tac aga gaa cca aga ggg cgt gtg aag atg atg tcc agt tta caa gca 192  
 Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala  
 50 55 60

cct ctt ctg aca att cag agc ttc tca ggg tta agg gcc ccc agt gca 240  
 Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala  
 65 70 75 80

tta gat tat ttg gga agg cct agt cca ggt ttc ctt gtt aag tat aaa 288  
 Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys  
 85 90 95

ctt gca aaa tca tct ggg aga gaa aaa gct agc cga tgt gta ccc aaa 336  
 Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys  
 100 105 110

gca atg ttt gag cgt ttt acc gag aaa gca att aag gtc ata atg ctg 384  
 Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu  
 115 120 125

tct	caa	gag	gaa	gct	cgg	aga	ctt	ggc	cat	aac	ttt	gtt	ggg	act	gag	432
Ser	Gln	Glu	Glu	Ala	Arg	Arg	Leu	Gly	His	Asn	Phe	Val	Gly	Thr	Glu	
	130						135				140					
caa	ata	ctg	ttg	ggg	cta	att	gga	gaa	ggg	act	ggg	att	gcc	gcc	aag	480
Gln	Ile	Leu	Leu	Gly	Leu	Ile	Gly	Glu	Gly	Thr	Gly	Ile	Ala	Ala	Lys	
	145				150					155					160	
gtt	ctt	aaa	tcc	atg	ggg	atc	aat	ctt	aaa	gat	tca	cgc	gtg	gaa	gta	528
Val	Leu	Lys	Ser	Met	Gly	Ile	Asn	Leu	Lys	Asp	Ser	Arg	Val	Glu	Val	
				165				170						175		
gaa	aag	ata	att	ggg	aga	ggc	agt	gga	ttc	gtg	gca	gtg	gag	att	cca	576
Glu	Lys	Ile	Ile	Gly	Arg	Gly	Ser	Gly	Phe	Val	Ala	Val	Glu	Ile	Pro	
		180					185						190			
ttt	act	cct	cgc	gca	aag	cgg	gtg	ctg	gag	ttg	tca	cta	gag	gaa	gct	624
Phe	Thr	Pro	Arg	Ala	Lys	Arg	Val	Leu	Glu	Leu	Ser	Leu	Glu	Glu	Ala	
	195						200					205				
cga	caa	ctt	ggg	cat	aac	tac	att	ggg	tca	gag	cac	ctt	ttg	ctt	ggg	672
Arg	Gln	Leu	Gly	His	Asn	Tyr	Ile	Gly	Ser	Glu	His	Leu	Leu	Leu	Gly	
	210					215					220					
cta	ctt	cgt	gaa	ggg	gag	ggg	gtg	gca	gct	cgt	gtc	ttg	gag	aat	ttg	720
Leu	Leu	Arg	Glu	Gly	Glu	Gly	Val	Ala	Ala	Arg	Val	Leu	Glu	Asn	Leu	
	225				230					235					240	
ggg	gca	gat	cct	agt	aat	ata	cgg	aca	cag	gtt	ata	cgt	atg	gtc	ggg	768
Gly	Ala	Asp	Pro	Ser	Asn	Ile	Arg	Thr	Gln	Val	Ile	Arg	Met	Val	Gly	
				245				250						255		
gaa	aac	aat	gaa	gtc	aca	gca	agc	gtt	ggg	ggg	gga	agc	agc	gga	aac	816
Glu	Asn	Asn	Glu	Val	Thr	Ala	Ser	Val	Gly	Gly	Gly	Ser	Ser	Gly	Asn	
			260					265					270			
agc	aaa	atg	cca	aca	ctt	gaa	gag	tat	ggg	act	aac	tta	act	aaa	cta	864
Ser	Lys	Met	Pro	Thr	Leu	Glu	Glu	Tyr	Gly	Thr	Asn	Leu	Thr	Lys	Leu	
	275					280						285				
gca	gag	gag	ggg	aaa	ctg	gat	cgg	gtt	gtt	gga	agg	cag	cca	cag	atc	912
Ala	Glu	Glu	Gly	Lys	Leu	Asp	Pro	Val	Val	Gly	Arg	Gln	Pro	Gln	Ile	
	290				295					300						
gaa	cga	atg	gtc	cag	atc	ttg	gct	cga	aga	acc	aag	aac	aac	cca	tgt	960
Glu	Arg	Met	Val	Gln	Ile	Leu	Ala	Arg	Arg	Thr	Lys	Asn	Asn	Pro	Cys	
	305				310					315					320	
ctt	att	gga	gaa	cct	gga	gtt	ggg	aag	acg	gca	ata	gca	gaa	gga	ctt	1008
Leu	Ile	Gly	Glu	Pro	Gly	Val	Gly	Lys	Thr	Ala	Ile	Ala	Glu	Gly	Leu	
				325				330						335		
gca	cag	cga	ata	gct	agt	ggg	gat	gtt	cct	gaa	aca	atc	gag	ggg	aag	1056
Ala	Gln	Arg	Ile	Ala	Ser	Gly	Asp	Val	Pro	Glu	Thr	Ile	Glu	Gly	Lys	
			340					345					350			
acg	gtt	ata	acc	ctt	gat	atg	ggg	ctt	cta	gtg	gct	gga	acg	aaa	tac	1104
Thr	Val	Ile	Thr	Leu	Asp	Met	Gly	Leu	Leu	Val	Ala	Gly	Thr	Lys	Tyr	
		355					360					365				

cgt gga gag ttc gag gaa aga ttg aag aag ctt atg gag gaa atc agg	1152
Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg	
370 375 380	
caa agt gat gag ata att ctg ttt att gat gaa gtg cac acg ctc atc	1200
Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile	
385 390 395 400	
ggt gca gga gcc gct gaa ggt gcg atc gat gct gct aac atc tta aag	1248
Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys	
405 410 415	
cca gct cta gca aga ggt gaa ttg cag tgt att ggt gca aca aca att	1296
Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile	
420 425 430	
gat gag tac agg aaa cac att gag aaa gat cct gca ttg gag aga cgg	1344
Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg	
435 440 445	
ttc cag cct gtg aaa gta cct gaa cca act gta gaa gaa gct ata cag	1392
Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln	
450 455 460	
att ttg caa ggt ctg cgt gag cgc tat gag atc cac cac aaa ctt cga	1440
Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg	
465 470 475 480	
tac act gat gaa gcc ttg gtt gct gct gca caa ttg tca cat cag tac	1488
Tyr Thr Asp Glu Ala Leu Val Ala Ala Ala Gln Leu Ser His Gln Tyr	
485 490 495	
atc agt gat cgg ttt ctt ccc gac aaa gcg att gac ttg att gat gaa	1536
Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu	
500 505 510	
gct ggg tct cgg gtt cga cta cgc cat gct cag ctt cct gag gaa gct	1584
Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala	
515 520 525	
aga gag ctt gaa aag caa ctc agg caa atc acc aaa gag aag aat gaa	1632
Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu	
530 535 540	
gct gtg cga agc caa gac ttc gag atg gct ggt tct cat cgt gac cgt	1680
Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg	
545 550 555 560	
gaa ata gag ctc aag gct gag ata gct aat gtt tta tct cga ggc aaa	1728
Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys	
565 570 575	
gaa gtg gcc aaa gcc gag aat gaa gct gag gaa gga gga cct act gtc	1776
Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val	
580 585 590	
aca gaa tct gac atc caa cac atc gtc gcc acc tgg aca gga atc ccg	1824
Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro	
595 600 605	



gta gag aaa gtc tcg tct gat gaa tct agc cgt ctt ctc caa atg gag Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu 610 615 620	1872
cag acc ctt cac aca aga gtc att ggc caa gat gaa gcc gtt aaa gca Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala 625 630 635 640	1920
atc agt cgg gct atc cgc cgt gcc cgt gtt ggg ctc aaa aac cca aac Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn 645 650 655	1968
cgt cct atc gcc agt ttc atc ttc tct ggt cca act ggt gtt ggg aaa Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys 660 665 670	2016
tca gag ctt gct aag gcc ttg gct gct tac tac ttc ggt tca gaa gaa Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu 675 680 685	2064
gca atg atc cgt ctt gac atg agt gag ttc atg gaa cga cac act gtt Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val 690 695 700	2112
tcg aaa ctc atc ggt tca cct cct ggt tac gta gga tac aca gaa gga Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly 705 710 715 720	2160
ggt cag tta aca gag gcg gtt cga cgc agg ccc tac act ctt gtt ctc Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Thr Leu Val Leu 725 730 735	2208
ttt gac gaa att gag aaa gca cat ccc gat gtt ttc aac atg atg ctt Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu 740 745 750	2256
cag atc cta gaa gac ggt aga cta act gat agc aaa gga aga act gtc Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val 755 760 765	2304
gat ttc aag aac acg ctt ctg atc atg act tca aac gta ggg agc agc Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser 770 775 780	2352
gtg atc gaa aaa ggt ggt aga aga att ggg ttt gat ctt gac cac gac Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp 785 790 795 800	2400
gag aaa gac agc agt tac aac aga atc aag agc tta gtg act gag gaa Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu 805 810 815	2448
cta aaa cag tat ttc aga cca gag ttc ttg aac agg tta gat gag atg Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met 820 825 830	2496
att gtt ttc aga cag tta aca aag ctg gaa gtc aag gag att gct gat Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp 835 840 845	2544

ata atg ctt aaa gaa gtg gtg gcg aga ctt gag gtc aaa gag att gag 2592  
 Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu  
 850 855 860

ctt cag gtg act gag agg ttt aaa gag aga gtg gtg gat gaa gga ttc 2640  
 Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe  
 865 870 875 880

gac ccg agt tat ggt gcg agg cca ctt aga cgt gca ata atg agg ctt 2688  
 Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu  
 885 890 895

ttg gag gat agt atg gcg gag aag atg ctt tca agg gac att aaa gaa 2736  
 Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu  
 900 905 910

gga gat tct gtg att gtt gat gtt gat gcc gaa gga agt gtg gtt gtg 2784  
 Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val  
 915 920 925

ttg agt ggt acc act gga cgt gtt ggt ggt ttt gct gct gaa gaa gcc 2832  
 Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala  
 930 935 940

atg gaa gat cct att cca ata ttg tag 2859  
 Met Glu Asp Pro Ile Pro Ile Leu  
 945 950

&lt;210&gt; 82

&lt;211&gt; 952

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 82

Met Ala Trp Ser Ile Ala Leu Leu Thr Pro Pro Phe Phe Gly Pro Gly  
 1 5 10 15

Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met  
 20 25 30

Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu  
 35 40 45

Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala  
 50 55 60

Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala  
 65 70 75 80

Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys  
85 90 95

Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys  
100 105 110

Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu  
115 120 125

Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu  
130 135 140

Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys  
145 150 155 160

Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val  
165 170 175

Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro  
180 185 190

Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala  
195 200 205

Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly  
210 215 220

Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu  
225 230 235 240

Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly  
245 250 255

Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Gly Ser Ser Gly Asn  
260 265 270

Ser Lys Met Pro Thr Leu Glu Glu Tyr Gly Thr Asn Leu Thr Lys Leu  
275 280 285

Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile  
290 295 300

Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys  
305 310 315 320

Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu  
 325 330 335

Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys  
 340 345 350

Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr  
 355 360 365

Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg  
 370 375 380

Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile  
 385 390 395 400

Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys  
 405 410 415

Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile  
 420 425 430

Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg  
 435 440 445

Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln  
 450 455 460

Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg  
 465 470 475 480

Tyr Thr Asp Glu Ala Leu Val Ala Ala Ala Gln Leu Ser His Gln Tyr  
 485 490 495

Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu  
 500 505 510

Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala  
 515 520 525

Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu  
 530 535 540

Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg  
 545 550 555 560

Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys  
565 570 575

Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val  
580 585 590

Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro  
595 600 605

Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu  
610 615 620

Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala  
625 630 635 640

Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn  
645 650 655

Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys  
660 665 670

Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu  
675 680 685

Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val  
690 695 700

Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly  
705 710 715 720

Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Thr Leu Val Leu  
725 730 735

Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu  
740 745 750

Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val  
755 760 765

Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser  
770 775 780

Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp  
785 790 795 800

Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu  
805 810 815

Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met  
820 825 830

Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp  
835 840 845

Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu  
850 855 860

Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe  
865 870 875 880

Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu  
885 890 895

Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu  
900 905 910

Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val  
915 920 925

Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala  
930 935 940

Met Glu Asp Pro Ile Pro Ile Leu  
945 950

<210> 83

<211> 1467

<212> DNA

<213> Arabidopsis thaliana

**<220>**

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att atc tct tct tct acc tct act atg cag aat ttg aag gag att gca 96  
 Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala  
 20 25 30

gca ctc atc gat act ggg tct tac acg aag gag gtt cgt cgt att gct 144  
 Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala  
 35 40 45

cgt gct gtg cgt ctc act ata ggg ctt agg cag aaa ctc acc ggc tct 192  
 Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser  
 50 55 60

gtg ctc tct tcc ttc ctg gat ttt gct ttg gtt cca gga tcc gaa gct 240  
 Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala  
 65 70 75 80

cac tct cgc ctc tct tcc ttt gtt cct aag ggt gat gaa cat gac atg 288  
 His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met  
 85 90 95

gaa gtt gat act gcc tca tcg gcc aca caa gct gct cct tct aag cat 336  
 Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His  
 100 105 110

cta cct gca gag ctc gag atc tac tgc tac ttc att gtt ctt ctt ttt 384  
 Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe  
 115 120 125

ctg att gat cag aag aag tac aac gag gct aaa gct tgt tct tca gca 432  
 Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala  
 130 135 140

agc att gct cgt ctc aag aac gtc aac cga agg acc att gat gtg ata 480  
 Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile  
 145 150 155 160

gca tca aga ctc tac ttt tac tat tct ttg agt tat gag caa acc ggt 528  
 Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly  
 165 170 175

gat ctt gct gaa att cgc ggt act ctt ctt gcg ttg cat cat tct gca 576  
 Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala  
 180 185 190

acg cta aga cac gat gag ctg ggt cag gaa acc ctt ctg aac ctg ttg 624  
 Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu  
 195 200 205

cta cgt aac tat ttg cat tac aac ctc tat gat cag gca gag aag cta 672  
 Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu  
 210 215 220

aga tca aag gca cct cgc ttt gag gct cat tca aac caa cag ttt tgt 720

Arg 225	Ser	Lys	Ala	Pro	Arg	Phe	Glu	Ala	His	Ser 235	Asn	Gln	Gln	Phe	Cys 240	
agg	tac	ctt	ttc	tat	ctc	ggg	aag	att	cgt	act	att	cag	ctc	gaa	tat	768
Arg	Tyr	Leu	Phe	Tyr	Leu	Gly	Lys	Ile	Arg 250	Thr	Ile	Gln	Leu	Glu	Tyr 255	
acg	gac	gca	aaa	gag	agc	ctt	ctt	cag	gcg	gcc	agg	aaa	gcc	cct	ata	816
Thr	Asp	Ala	Lys	Glu	Ser	Leu	Leu	Gln	Ala	Ala	Arg	Lys	Ala	Pro	Ile 270	
gca	gct	ttg	ggc	ttc	agg	atc	caa	tgc	aat	aaa	tgg	gca	att	ctg	gtt	864
Ala	Ala	Leu	Gly	Phe	Arg	Ile	Gln	Cys	Asn	Lys	Trp	Ala	Ile	Leu	Val 285	
cgt	cta	ctg	ctg	ggg	gag	ata	cca	gag	cgt	tct	atc	ttc	act	caa	aag	912
Arg	Leu	Leu	Leu	Gly	Glu	Ile	Pro	Glu	Arg	Ser	Ile	Phe	Thr	Gln	Lys 300	
ggg	atg	gag	aag	gcc	ctc	aga	ccc	tac	ttc	gag	cta	aca	aat	gcg	gtt	960
Gly	Met	Glu	Lys	Ala	Leu	Arg	Pro	Tyr	Phe	Glu	Leu	Thr	Asn	Ala	Val 320	
agg	att	ggg	gac	ttg	gag	ttg	ttt	agg	aca	gtc	cag	gag	aag	ttc	ttg	1008
Arg	Ile	Gly	Asp	Leu	Glu	Leu	Phe	Arg	Thr	Val	Gln	Glu	Lys	Phe	Leu 335	
gac	aca	ttt	gct	caa	gac	aga	acg	cac	aat	ctc	atc	gtg	cga	ctc	cgc	1056
Asp	Thr	Phe	Ala	Gln	Asp	Arg	Thr	His	Asn	Leu	Ile	Val	Arg	Leu	Arg 350	
cac	aat	gtc	atc	agg	act	gga	ctg	cgg	aac	ata	agt	atc	tcc	tac	tca	1104
His	Asn	Val	Ile	Arg	Thr	Gly	Leu	Arg	Asn	Ile	Ser	Ile	Ser	Tyr	Ser 365	
aga	atc	tct	tta	ccc	gat	gtt	gcc	aaa	aag	ctg	agg	ctc	aac	tct	gaa	1152
Arg	Ile	Ser	Leu	Pro	Asp	Val	Ala	Lys	Lys	Leu	Arg	Leu	Asn	Ser	Glu 380	
aac	cct	gtg	gct	gat	gcg	gaa	agc	atc	gtg	gca	aag	gcc	ata	cgc	gac	1200
Asn	Pro	Val	Ala	Asp	Ala	Glu	Ser	Ile	Val	Ala	Lys	Ala	Ile	Arg	Asp 400	
gga	gct	att	gat	gct	aca	atc	gat	cac	aaa	aac	gga	tgc	atg	gtc	tcc	1248
Gly	Ala	Ile	Asp	Ala	Thr	Ile	Asp	His	Lys	Asn	Gly	Cys	Met	Val	Ser 415	
aaa	gaa	act	ggg	gac	atc	tac	tcg	acg	aat	gag	cca	caa	act	gcg	ttc	1296
Lys	Glu	Thr	Gly	Asp	Ile	Tyr	Ser	Thr	Asn	Glu	Pro	Gln	Thr	Ala	Phe 430	
aac	tca	aga	att	gct	ttc	tgc	ctc	aac	atg	cat	aac	gaa	gct	gtc	aga	1344
Asn	Ser	Arg	Ile	Ala	Phe	Cys	Leu	Asn	Met	His	Asn	Glu	Ala	Val	Arg 445	
gca	ttg	agg	ttt	cct	cct	aac	act	cac	aag	gag	aaa	gaa	agc	gat	gag	1392
Ala	Leu	Arg	Phe	Pro	Pro	Asn	Thr	His	Lys	Glu	Lys	Glu	Ser	Asp	Glu 460	
aag	agg	aga	gag	agg	aag	caa	cag	gaa	gaa	gag	ctt	gct	aag	cat	atg	1440



Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met  
 465 470 475 480

gct gag gaa gac gat gat gat ttt tag  
 Ala Glu Glu Asp Asp Asp Asp Phe  
 485

1467

&lt;210&gt; 84

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 84

Met Thr Gln Asp Val Glu Met Lys Asp Asn Asn Thr Pro Ser Gln Ser  
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Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala  
 20 25 30

Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala  
 35 40 45

Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser  
 50 55 60

Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala  
 65 70 75 80

His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met  
 85 90 95

Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His  
 100 105 110

Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe  
 115 120 125

Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala  
 130 135 140

Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile  
 145 150 155 160

Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly  
 165 170 175

Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala  
 180 185 190

Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu  
 195 200 205

Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu  
 210 215 220

Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys  
 225 230 235 240

Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr  
 245 250 255

Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile  
 260 265 270

Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val  
 275 280 285

Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys  
 290 295 300

Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val  
 305 310 315 320

Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu  
 325 330 335

Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg  
 340 345 350

His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Ile Ser Tyr Ser  
 355 360 365

Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu  
 370 375 380

Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp  
 385 390 395 400

Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser  
405 410 415

Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe  
420 425 430

Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg  
435 440 445

Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Glu Ser Asp Glu  
450 455 460

Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met  
465 470 475 480

Ala Glu Glu Asp Asp Asp Asp Phe  
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<210> 85

<211> 282

<212> DNA

<213> Arabidopsis thaliana

**<220>**

<221> CDS

<222> (1) .. (282)

<223> 68181

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1          5          10          15

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aaa gcc aaa atg gcc tcc atg atc gat cag ctt cag ctc cgt gat agt 96  
Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser  
20 25 30

ttg agg atg tac aat tca ttg gtg gag agg tgt ttc gtg gac tgt gtt 144  
Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val  
35 40 45

gat agc ttc aca cgc aaa tct ctg cag aaa caa gag gag act tgt gtg 192  
Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val  
50 55 60

atg cgt tgc gct gag aag ttc ctt aag cat acg atg cgt gtt ggt atg 240  
 Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met  
 65 70 75 80

cgg ttt gct gag ctc aat cag aac gca cca acc caa gac tga 282  
 Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp  
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<210> 86

<211> 93

<212> PRT

<213> Arabidopsis thaliana

<400> 86

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Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser  
 20 25 30

Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val  
 35 40 45

Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val  
 50 55 60

Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met  
 65 70 75 80

Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp  
 85 90

<210> 87

<211> 816

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

&lt;222&gt; (1) .. (816)

&lt;223&gt; 70913

&lt;400&gt; 87

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Met	Gln	Ser	Lys	Pro	Gly	Arg	Glu	Asn	Glu	Glu	Glu	Val	Asn	Asn	His	
1				5					10					15		

cat	gct	gtt	cag	cag	ccg	atg	atg	tat	gca	gag	ccc	tgg	tgg	aaa	aac	96
His	Ala	Val	Gln	Gln	Pro	Met	Met	Tyr	Ala	Glu	Pro	Trp	Trp	Lys	Asn	
			20					25					30			

aac	tcc	ttt	ggt	gtt	gta	cct	caa	gcg	aga	cct	tct	gga	att	cca	tca	144
Asn	Ser	Phe	Gly	Val	Val	Pro	Gln	Ala	Arg	Pro	Ser	Gly	Ile	Pro	Ser	
		35					40					45				

aat	tcc	tct	tct	ttg	gat	tgc	ccc	aat	ggt	tcc	gag	tca	aac	gat	gtt	192
Asn	Ser	Ser	Ser	Leu	Asp	Cys	Pro	Asn	Gly	Ser	Glu	Ser	Asn	Asp	Val	
	50					55					60					

cat	tca	gca	tct	gaa	gac	ggt	gcg	ttg	aat	ggt	gaa	aac	gat	ggc	act	240
His	Ser	Ala	Ser	Glu	Asp	Gly	Ala	Leu	Asn	Gly	Glu	Asn	Asp	Gly	Thr	
65					70					75					80	

tgg	aag	gat	tca	caa	gct	gca	act	tcc	tct	cgt	tca	gat	aat	cac	gga	288
Trp	Lys	Asp	Ser	Gln	Ala	Ala	Thr	Ser	Ser	Arg	Ser	Asp	Asn	His	Gly	
				85					90					95		

atg	gaa	gga	aat	gac	cca	gcg	ctc	tct	atc	cgt	aac	atg	cat	gat	cag	336
Met	Glu	Gly	Asn	Asp	Pro	Ala	Leu	Ser	Ile	Arg	Asn	Met	His	Asp	Gln	
			100					105					110			

cca	ctt	gta	caa	cca	cca	gag	ctt	gtt	gga	cac	tat	atc	gct	tgt	gtc	384
Pro	Leu	Val	Gln	Pro	Pro	Glu	Leu	Val	Gly	His	Tyr	Ile	Ala	Cys	Val	
		115					120					125				

cca	aac	cca	tat	cag	gat	cca	tat	tat	ggg	gga	ttg	atg	gga	gca	tat	432
Pro	Asn	Pro	Tyr	Gln	Asp	Pro	Tyr	Tyr	Gly	Gly	Leu	Met	Gly	Ala	Tyr	
	130					135					140					

ggt	cat	cag	caa	ttg	ggt	ttt	cgt	cca	tat	ctt	gga	atg	cct	cgt	gaa	480
Gly	His	Gln	Gln	Leu	Gly	Phe	Arg	Pro	Tyr	Leu	Gly	Met	Pro	Arg	Glu	
145					150					155					160	

aga	aca	gct	ctg	cca	ctt	gac	atg	gca	caa	gag	ccc	gtt	tat	gtg	aat	528
Arg	Thr	Ala	Leu	Pro	Leu	Asp	Met	Ala	Gln	Glu	Pro	Val	Tyr	Val	Asn	
			165					170						175		

gca	aag	cag	tac	gag	gga	att	cta	agg	cga	aga	aaa	gca	cgt	gcc	aag	576
Ala	Lys	Gln	Tyr	Glu	Gly	Ile	Leu	Arg	Arg	Arg	Lys	Ala	Arg	Ala	Lys	
		180					185					190				

gca	gag	cta	gag	agg	aaa	gtc	atc	cgg	gac	aga	aag	cca	tat	ctt	cac	624
Ala	Glu	Leu	Glu	Arg	Lys	Val	Ile	Arg	Asp	Arg	Lys	Pro	Tyr	Leu	His	
		195				200						205				

gag	tca	aga	cac	aag	cat	gca	atg	aga	agg	gca	cga	gcg	agt	gga	ggc	672
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly  
 210 215 220  
 cgg ttt gcg aag aaa agt gag gta gaa gcg gga gag gat gca gga ggg 720  
 Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly  
 225 230 235 240  
 aga gac aga gaa agg ggt tca gca acc aac tca tca ggc tct gaa caa 768  
 Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln  
 245 250 255  
 gtt gag aca gac tct aat gag acc ctg aat tct tct ggt gca cca taa 816  
 Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro  
 260 265 270

<210> 88

<211> 271

<212> PRT

<213> Arabidopsis thaliana

<400> 88

Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His  
 1 5 10 15  
 His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn  
 20 25 30  
 Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser  
 35 40 45  
 Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val  
 50 55 60  
 His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr  
 65 70 75 80  
 Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly  
 85 90 95  
 Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln  
 100 105 110  
 Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val  
 115 120 125

Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr  
 130 135 140

Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu  
 145 150 155 160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn  
 165 170 175

Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys  
 180 185 190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His  
 195 200 205

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly  
 210 215 220

Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly  
 225 230 235 240

Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln  
 245 250 255

Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro  
 260 265 270

<210> 89

<211> 990

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(990)

<223> 71067

<400> 89

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 Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu  
 1 5 10 15

48

tct gac ggt ttt gat tat ccc gac ggt atc cca ata tca tac aat ctt Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu 20 25 30	96
cat agg ctt cgt cac ttt gag tgt gaa ggc agt tat ccc aag tat cct His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro 35 40 45	144
tat ggt tct ttg gtc aag ttt tat gca atg gtg gga ctt cat cgt tac Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr 50 55 60	192
aat gtg ttg gag ggg aaa aat ttg cag ctc gat acc cta aag agt ttc Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe 65 70 75 80	240
aac atg aga atc aat tgt ggt gct tct tct tac tac att act ttg gct Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala 85 90 95	288
gca cgc gtt cca gat agc ggt ttg aag cag atc ttt cag gtt cta gtt Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val 100 105 110	336
cat gaa gag cgt ctt ggc agt tta gac atg aca tgt act atc gct aga His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg 115 120 125	384
cct cga gtg act acc aat gtg cct ttt cta cgt ccg cac agc gaa tca Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser 130 135 140	432
gag tat gat tat atg gac aat gat gaa ttg cct gac tgg cct tca gag Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu 145 150 155 160	480
att gct ttc gat gat aca aaa cgg ttt cat ctg gtg aag gaa tca gag Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu 165 170 175	528
ttg cga gac aat gat tgg att cga ctc tat ttg gaa ctt aca ctt gtt Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val 180 185 190	576
gct cac gat agg ttt ctt aca gtt cac tat ctc tcc cag ttg gag att Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile 195 200 205	624
gtg aaa gtt gcg att gaa gaa gtg gag caa ccg aat gcg agt ctc aac Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn 210 215 220	672
acc aaa act aca ttt gtc tac ata act tat aag gac ttg gca aag gct Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala 225 230 235 240	720
cag att ggt gag ccg gtt gat cgc aaa gct att gtt aga aaa atc atc Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile 245 250 255	768



aat gag act acg gga ctc ttg aga ctc cgg ggt gat tat tgg agt gga 816  
 Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly  
 260 265 270  
  
 gaa aga agt gtg atc act ccg gag gag gaa tat atg ctt ctc cat ggc 864  
 Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly  
 275 280 285  
  
 gga gaa aaa gtt cga aac aat gag cag cgt tct aaa aaa ctt aag cgt 912  
 Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg  
 290 295 300  
  
 cgt gta ggt gtt cat agg cta tgg cga tgg tgg tac cag gct tac aaa 960  
 Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys  
 305 310 315 320  
  
 aac cgt ggc ctc cgc tcg tcg tct tat taa 990  
 Asn Arg Gly Leu Arg Ser Ser Ser Tyr  
 325

&lt;210&gt; 90

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 90

Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu  
 1 5 10 15

Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu  
 20 25 30

His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro  
 35 40 45

Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr  
 50 55 60

Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe  
 65 70 75 80

Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala  
 85 90 95

Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val  
 100 105 110

His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg  
 115 120 125

Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser  
 130 135 140

Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu  
 145 150 155 160

Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu  
 165 170 175

Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val  
 180 185 190

Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile  
 195 200 205

Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn  
 210 215 220

Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala  
 225 230 235 240

Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile  
 245 250 255

Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly  
 260 265 270

Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly  
 275 280 285

Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg  
 290 295 300

Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys  
 305 310 315 320

Asn Arg Gly Leu Arg Ser Ser Ser Tyr  
 325

<210> 91

&lt;211&gt; 1614

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1614)

&lt;223&gt; 71654

&lt;400&gt; 91

atg gcg ctc gtg aaa acg gaa acg cag gcg tta gga aac cac cag cat	48
Met Ala Leu Val Lys Thr Glu Thr Gln Ala Leu Gly Asn His Gln His	
1 5 10 15	

tct tca agg ttt ggt tcg ctt tac gtc ggt gat ctt agc cca gac gtg	96
Ser Ser Arg Phe Gly Ser Leu Tyr Val Gly Asp Leu Ser Pro Asp Val	
20 25 30	

acg gag aaa gat ctc att gat aag ttc tct ttg aat gtt ccg gta gtg	144
Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val	
35 40 45	

tcc gtt cat ctt tgc cgt aac tct gtc acc gga aaa tcc atg tgt tac	192
Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr	
50 55 60	

gct tac atc aac ttc gat tca cct ttc agc gca tcg aat gct atg act	240
Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr	
65 70 75 80	

cgc tta aac cat agt gat ttg aag gga aag gct atg cga ata atg tgg	288
Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp	
85 90 95	

tct cag agg gat ctt gcg tac cgt cgt cgt act cgt act ggt ttt gca	336
Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala	
100 105 110	

aat cta tac gta aag aat ctg gat agc tcg att act agc agt tgc tta	384
Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu	
115 120 125	

gag cga atg ttt tgc ccc ttt ggt tcc ata ctt tct tgc aaa gtc gtt	432
Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val	
130 135 140	

gaa gag aat ggc caa agt aaa ggt ttt ggc ttt gtt cag ttt gat aca	480
Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr	
145 150 155 160	

gag caa tct gct gta tct gct cgt tct gct ctc cac ggc tct atg gtt	528
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Glu	Gln	Ser	Ala	Val	Ser	Ala	Arg	Ser	Ala	Leu	His	Gly	Ser	Met	Val	
				165					170					175		
tat	ggc	aag	aaa	ctg	ttt	gtt	gcc	aag	ttc	atc	aac	aag	gat	gaa	aga	576
Tyr	Gly	Lys	Lys	Leu	Phe	Val	Ala	Lys	Phe	Ile	Asn	Lys	Asp	Glu	Arg	
			180					185					190			
gca	gct	atg	gca	gga	aat	caa	gac	tct	aca	aac	gtt	tat	gtg	aag	aat	624
Ala	Ala	Met	Ala	Gly	Asn	Gln	Asp	Ser	Thr	Asn	Val	Tyr	Val	Lys	Asn	
		195					200					205				
ctg	atc	gaa	act	gtt	aca	gat	gat	tgt	cta	cat	aca	ctg	ttt	tct	caa	672
Leu	Ile	Glu	Thr	Val	Thr	Asp	Asp	Cys	Leu	His	Thr	Leu	Phe	Ser	Gln	
	210					215					220					
tat	gga	act	gtc	tct	agt	gtt	gtg	gtt	atg	agg	gat	ggg	atg	gga	aga	720
Tyr	Gly	Thr	Val	Ser	Ser	Val	Val	Val	Met	Arg	Asp	Gly	Met	Gly	Arg	
225					230				235						240	
tct	aga	ggg	ttc	gga	ttt	gtt	aac	ttc	tgc	aat	cca	gaa	aat	gct	aag	768
Ser	Arg	Gly	Phe	Gly	Phe	Val	Asn	Phe	Cys	Asn	Pro	Glu	Asn	Ala	Lys	
			245					250						255		
aaa	gct	atg	gaa	tct	ctc	tgt	gga	cta	caa	ctt	gga	tcg	aag	aaa	ttg	816
Lys	Ala	Met	Glu	Ser	Leu	Cys	Gly	Leu	Gln	Leu	Gly	Ser	Lys	Lys	Leu	
		260					265					270				
ttt	gtt	ggg	aag	gca	ctc	aag	aaa	gat	gaa	agg	agg	gag	atg	ctg	aaa	864
Phe	Val	Gly	Lys	Ala	Leu	Lys	Lys	Asp	Glu	Arg	Arg	Glu	Met	Leu	Lys	
		275				280						285				
cag	aaa	ttc	agt	gac	aac	ttt	att	gca	aag	cct	aac	atg	aga	tgg	tcc	912
Gln	Lys	Phe	Ser	Asp	Asn	Phe	Ile	Ala	Lys	Pro	Asn	Met	Arg	Trp	Ser	
	290				295					300						
aat	ctg	tac	gtg	aag	aac	ttg	agt	gaa	tca	atg	aat	gaa	aca	aga	ctg	960
Asn	Leu	Tyr	Val	Lys	Asn	Leu	Ser	Glu	Ser	Met	Asn	Glu	Thr	Arg	Leu	
305					310				315						320	
cga	gaa	atc	ttt	gga	tgc	tat	ggg	caa	ata	gtt	tca	gct	aaa	gtg	atg	1008
Arg	Glu	Ile	Phe	Gly	Cys	Tyr	Gly	Gln	Ile	Val	Ser	Ala	Lys	Val	Met	
			325					330						335		
tgt	cat	gag	aat	ggc	aga	agt	aaa	gga	ttc	ggc	ttt	gtg	tgc	ttc	tct	1056
Cys	His	Glu	Asn	Gly	Arg	Ser	Lys	Gly	Phe	Gly	Phe	Val	Cys	Phe	Ser	
		340					345					350				
aac	tgt	gaa	gag	tcc	aaa	cag	gct	aaa	aga	tat	ctc	aat	ggg	ttc	tta	1104
Asn	Cys	Glu	Glu	Ser	Lys	Gln	Ala	Lys	Arg	Tyr	Leu	Asn	Gly	Phe	Leu	
		355				360					365					
gtt	gat	gga	aag	cca	ata	gtt	gtt	cga	gtt	gca	gag	cgc	aaa	gag	gat	1152
Val	Asp	Gly	Lys	Pro	Ile	Val	Val	Arg	Val	Ala	Glu	Arg	Lys	Glu	Asp	
	370					375				380						
cga	atc	aag	agg	ttg	cag	caa	tat	ttt	cag	gca	cag	cca	cgc	cag	tac	1200
Arg	Ile	Lys	Arg	Leu	Gln	Gln	Tyr	Phe	Gln	Ala	Gln	Pro	Arg	Gln	Tyr	
385					390					395					400	
acg	caa	gct	cct	tct	gcc	cct	tca	cca	gct	cag	cca	gtc	ctc	tca	tat	1248

Thr	Gln	Ala	Pro	Ser	Ala	Pro	Ser	Pro	Ala	Gln	Pro	Val	Leu	Ser	Tyr		
				405					410					415			
gtg	tcc	agc	tca	tat	ggg	tgc	ttt	cag	cca	ttc	cag	gtc	ggg	aca	tct		1296
Val	Ser	Ser	Ser	Tyr	Gly	Cys	Phe	Gln	Pro	Phe	Gln	Val	Gly	Thr	Ser		
				420				425					430				
tat	tac	tat	atg	ggc	aat	cag	gtg	cca	caa	atg	tcc	ggg	cac	caa	aac		1344
Tyr	Tyr	Tyr	Met	Gly	Asn	Gln	Val	Pro	Gln	Met	Ser	Gly	His	Gln	Asn		
				435				440					445				
atc	acc	acc	tac	gtt	cca	gct	ggg	aaa	gtg	cct	ctc	aag	gag	aga	aga		1392
Ile	Thr	Thr	Tyr	Val	Pro	Ala	Gly	Lys	Val	Pro	Leu	Lys	Glu	Arg	Arg		
				450				455					460				
tca	atg	cat	ctg	gtc	tac	aaa	cat	ccg	gct	tat	ccc	gtt	gcc	aag	agg		1440
Ser	Met	His	Leu	Val	Tyr	Lys	His	Pro	Ala	Tyr	Pro	Val	Ala	Lys	Arg		
				465				470					475				480
ggg	gct	aaa	cag	aca	ctg	gtt	ttt	aag	ggg	gag	gtt	aac	aga	aac	tta		1488
Gly	Ala	Lys	Gln	Thr	Leu	Val	Phe	Lys	Gly	Glu	Val	Asn	Arg	Asn	Leu		
				485													495
gag	gct	gca	aca	tgc	tcc	aaa	gca	aca	aca	tct	gag	gag	aac	cgt	aaa		1536
Glu	Ala	Ala	Thr	Cys	Ser	Lys	Ala	Thr	Thr	Ser	Glu	Glu	Asn	Arg	Lys		
				500				505					510				
gaa	gaa	cga	aga	ttg	act	ttg	tca	gga	aag	ttg	tca	cca	gaa	gtg	aag		1584
Glu	Glu	Arg	Arg	Leu	Thr	Leu	Ser	Gly	Lys	Leu	Ser	Pro	Glu	Val	Lys		
				515				520				525					
gta	gag	gaa	tca	gga	aaa	caa	ttg	caa	tga								1614
Val	Glu	Glu	Ser	Gly	Lys	Gln	Leu	Gln									
				530				535									

&lt;210&gt; 92

&lt;211&gt; 537

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 92

Met	Ala	Leu	Val	Lys	Thr	Glu	Thr	Gln	Ala	Leu	Gly	Asn	His	Gln	His		
1				5					10					15			
Ser	Ser	Arg	Phe	Gly	Ser	Leu	Tyr	Val	Gly	Asp	Leu	Ser	Pro	Asp	Val		
				20				25					30				
Thr	Glu	Lys	Asp	Leu	Ile	Asp	Lys	Phe	Ser	Leu	Asn	Val	Pro	Val	Val		
				35			40					45					

Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr  
 50 55 60

Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr  
 65 70 75 80

Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp  
 85 90 95

Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala  
 100 105 110

Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu  
 115 120 125

Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val  
 130 135 140

Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr  
 145 150 155 160

Glu Gln Ser Ala Val Ser Ala Arg Ser Ala Leu His Gly Ser Met Val  
 165 170 175

Tyr Gly Lys Lys Leu Phe Val Ala Lys Phe Ile Asn Lys Asp Glu Arg  
 180 185 190

Ala Ala Met Ala Gly Asn Gln Asp Ser Thr Asn Val Tyr Val Lys Asn  
 195 200 205

Leu Ile Glu Thr Val Thr Asp Asp Cys Leu His Thr Leu Phe Ser Gln  
 210 215 220

Tyr Gly Thr Val Ser Ser Val Val Val Met Arg Asp Gly Met Gly Arg  
 225 230 235 240

Ser Arg Gly Phe Gly Phe Val Asn Phe Cys Asn Pro Glu Asn Ala Lys  
 245 250 255

Lys Ala Met Glu Ser Leu Cys Gly Leu Gln Leu Gly Ser Lys Lys Leu  
 260 265 270

Phe Val Gly Lys Ala Leu Lys Lys Asp Glu Arg Arg Glu Met Leu Lys  
 275 280 285

Gln Lys Phe Ser Asp Asn Phe Ile Ala Lys Pro Asn Met Arg Trp Ser  
 290 295 300

Asn Leu Tyr Val Lys Asn Leu Ser Glu Ser Met Asn Glu Thr Arg Leu  
 305 310 315 320

Arg Glu Ile Phe Gly Cys Tyr Gly Gln Ile Val Ser Ala Lys Val Met  
 325 330 335

Cys His Glu Asn Gly Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser  
 340 345 350

Asn Cys Glu Glu Ser Lys Gln Ala Lys Arg Tyr Leu Asn Gly Phe Leu  
 355 360 365

Val Asp Gly Lys Pro Ile Val Val Arg Val Ala Glu Arg Lys Glu Asp  
 370 375 380

Arg Ile Lys Arg Leu Gln Gln Tyr Phe Gln Ala Gln Pro Arg Gln Tyr  
 385 390 395 400

Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr  
 405 410 415

Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser  
 420 425 430

Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn  
 435 440 445

Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg  
 450 455 460

Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg  
 465 470 475 480

Gly Ala Lys Gln Thr Leu Val Phe Lys Gly Glu Val Asn Arg Asn Leu  
 485 490 495

Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys  
 500 505 510

Glu Glu Arg Arg Leu Thr Leu Ser Gly Lys Leu Ser Pro Glu Val Lys  
 515 520 525

Val Glu Glu Ser Gly Lys Gln Leu Gln  
530 535

<210> 93

<211> 657

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(657)

<223> ET3172

<400> 93

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gaa gaa caa cac tat tct tta tca aga ctc tcc gtt tgt tcc aac tac	96
Glu Glu Gln His Tyr Ser Leu Ser Arg Leu Ser Val Cys Ser Asn Tyr	
20 25 30	

gac ggc gat gaa gcc gac ggt gag tct tct gct tcc gac gag aaa cgt	144
Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg	
35 40 45	

gtt gtc cac ggc gga gga gag aaa tcc atg gag gag cta aat ttt tca	192
Val Val His Gly Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser	
50 55 60	

gat tct gat aaa gaa tca acc ggt tgt caa tct ctc ccg gcg aca cct	240
Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro	
65 70 75 80	

ccg aga cgg aga cgg cgg aga ggc ggt gga gga gga gga tat tta gcg	288
Pro Arg Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Gly Tyr Leu Ala	
85 90 95	

gtg agt tct ccg gtt tcc ggc gat aaa gct tac gct agc gag aac gaa	336
Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu	
100 105 110	

gta caa aag acg aat aac aat cag agg aga agg agg aga ttg aaa ccg	384
Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro	
115 120 125	

gag tgt cca ccg tgg gtt gat agt atg cgg agg agc tac gtc gga gat	432
Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp	
130 135 140	



gaa cag agt agt cac ggt ggt tac gga gga gga gtg gtg gtt gtt acg 480  
 Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Gly Val Val Val Val Thr  
 145 150 155 160  
 agg cct ata gga gga gga agg cca ttg tgt atg gat tta gaa gaa gtc 528  
 Arg Pro Ile Gly Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val  
 165 170 175  
 aaa gct tgt aaa gat ttg ggg ttt gag ctt gaa ccg ggt cgg gtt tcg 576  
 Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser  
 180 185 190  
 tat tcc ggg tca acg gtg gat act agt agt ggc ggc aat tct cct atc 624  
 Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile  
 195 200 205  
 tct tct aac cac cgt att tcg agt ccc ggt tag 657  
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 20 25 30  
 Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg  
 35 40 45  
 Val Val His Gly Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser  
 50 55 60  
 Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro  
 65 70 75 80  
 Pro Arg Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Tyr Leu Ala  
 85 90 95  
 Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu  
 100 105 110

Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro  
 115 120 125

Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp  
 130 135 140

Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Gly Val Val Val Val Thr  
 145 150 155 160

Arg Pro Ile Gly Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val  
 165 170 175

Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser  
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Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile  
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Ser Ser Asn His Arg Ile Ser Ser Pro Gly  
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 1 5 10 15

gtc tac aaa aat gct att ttc atg tgc gag cgt ctc tgc gct gag ttt 96  
 Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe  
 20 25 30

cct tct gag gtt aat ttg cag cta tta gcc acc agc tac ctg cag aat 144

Pro	Ser	Glu	Val	Asn	Leu	Gln	Leu	Leu	Ala	Thr	Ser	Tyr	Leu	Gln	Asn	
		35					40					45				
aat	caa	gct	tac	agt	gca	tat	cat	ctg	cta	aag	gga	aca	caa	atg	gct	192
Asn	Gln	Ala	Tyr	Ser	Ala	Tyr	His	Leu	Leu	Lys	Gly	Thr	Gln	Met	Ala	
		50				55					60					
cag	tcc	cga	tac	ttg	ttc	gca	tta	tca	tgc	ttc	cag	atg	gac	ctt	ctc	240
Gln	Ser	Arg	Tyr	Leu	Phe	Ala	Leu	Ser	Cys	Phe	Gln	Met	Asp	Leu	Leu	
65					70					75				80		
aat	gaa	gct	gaa	tct	gca	ctc	tgc	cct	gtt	aat	gaa	cct	ggt	gcg	gag	288
Asn	Glu	Ala	Glu	Ser	Ala	Leu	Cys	Pro	Val	Asn	Glu	Pro	Gly	Ala	Glu	
				85					90					95		
atc	cca	aat	ggt	gca	gca	ggc	cat	tac	ctt	ctt	gga	ctt	att	tac	aag	336
Ile	Pro	Asn	Gly	Ala	Ala	Gly	His	Tyr	Leu	Leu	Gly	Leu	Ile	Tyr	Lys	
			100					105					110			
aag	aat	gct	gct	caa	caa	ttt	aaa	cag	tcc	ttg	aca	ata	gac	cct	cta	384
Lys	Asn	Ala	Ala	Gln	Gln	Phe	Lys	Gln	Ser	Leu	Thr	Ile	Asp	Pro	Leu	
		115					120					125				
ctt	tgg	gct	gca	tat	gag	gaa	tta	tgt	ata	tta	ggt	gct	gct	gag	gaa	432
Leu	Trp	Ala	Ala	Tyr	Glu	Glu	Leu	Cys	Ile	Leu	Gly	Ala	Ala	Glu	Glu	
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gca	act	gca	gtt	ttt	ggt	gaa	aca	gct	gct	ctc	tcc	att	caa	aag	cag	480
Ala	Thr	Ala	Val	Phe	Gly	Glu	Thr	Ala	Ala	Leu	Ser	Ile	Gln	Lys	Gln	
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tat	atg	caa	caa	ctg	tca	act	tcc	ctc	ggc	tta	aac	act	tac	aac	gag	528
Tyr	Met	Gln	Gln	Leu	Ser	Thr	Ser	Leu	Gly	Leu	Asn	Thr	Tyr	Asn	Glu	
				165					170					175		
gaa	cgt	aat	tca	act	tct	act	aaa	aac	acg	agt	tct	gaa	gat	tat	agt	576
Glu	Arg	Asn	Ser	Thr	Ser	Thr	Lys	Asn	Thr	Ser	Ser	Glu	Asp	Tyr	Ser	
			180					185					190			
cca	agg	cag	tct	aaa	cac	aca	caa	agc	cat	ggc	ctt	aaa	gat	atc	tcc	624
Pro	Arg	Gln	Ser	Lys	His	Thr	Gln	Ser	His	Gly	Leu	Lys	Asp	Ile	Ser	
		195					200					205				
gga	aat	ttc	cat	tct	cat	gga	gtt	aat	gga	ggt	gtt	tcg	aac	atg	tca	672
Gly	Asn	Phe	His	Ser	His	Gly	Val	Asn	Gly	Gly	Val	Ser	Asn	Met	Ser	
	210					215					220					
ttc	tat	aat	acg	cct	tcg	cca	gtg	gct	gca	cag	cta	tcc	ggt	ata	gct	720
Phe	Tyr	Asn	Thr	Pro	Ser	Pro	Val	Ala	Ala	Gln	Leu	Ser	Gly	Ile	Ala	
225					230					235					240	
cca	cca	cca	ctt	ttc	cgg	aat	ttt	cag	cca	gct	gtt	gca	aac	cca	aac	768
Pro	Pro	Pro	Leu	Phe	Arg	Asn	Phe	Gln	Pro	Ala	Val	Ala	Asn	Pro	Asn	
				245					250					255		
tcc	ctt	att	act	gac	agt	tct	cca	aag	tcc	act	gtt	aac	tct	act	ctt	816
Ser	Leu	Ile	Thr	Asp	Ser	Ser	Pro	Lys	Ser	Thr	Val	Asn	Ser	Thr	Leu	
			260					265					270			
caa	gca	cct	aga	aga	aag	ttt	gta	gat	gaa	gga	aag	tta	cgt	aag	att	864

Gln	Ala	Pro	Arg	Arg	Lys	Phe	Val	Asp	Glu	Gly	Lys	Leu	Arg	Lys	Ile	
	275						280					285				
tct	ggc	aga	cta	ttt	tct	gat	tct	ggc	cca	cga	cgg	agt	tca	aga	ctg	912
Ser	Gly	Arg	Leu	Phe	Ser	Asp	Ser	Gly	Pro	Arg	Arg	Ser	Ser	Arg	Leu	
	290					295					300					
tct	gct	gat	tca	ggg	gca	aac	att	aat	tca	agt	gtt	gca	aca	gta	agc	960
Ser	Ala	Asp	Ser	Gly	Ala	Asn	Ile	Asn	Ser	Ser	Val	Ala	Thr	Val	Ser	
	305				310					315					320	
gga	aat	gtg	aac	aac	gct	tcc	aag	tat	ttg	gga	ggc	tct	aaa	ttg	agt	1008
Gly	Asn	Val	Asn	Asn	Ala	Ser	Lys	Tyr	Leu	Gly	Gly	Ser	Lys	Leu	Ser	
			325						330					335		
tct	ttg	gca	ctt	cgt	tct	gta	aca	ctt	cgg	aag	gga	cac	tcc	tgg	gca	1056
Ser	Leu	Ala	Leu	Arg	Ser	Val	Thr	Leu	Arg	Lys	Gly	His	Ser	Trp	Ala	
			340					345					350			
aat	gaa	aac	atg	gat	gaa	ggg	gtc	cgt	ggg	gaa	cct	ttt	gat	gat	tca	1104
Asn	Glu	Asn	Met	Asp	Glu	Gly	Val	Arg	Gly	Glu	Pro	Phe	Asp	Asp	Ser	
	355						360					365				
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Arg	Pro	Asn	Thr	Ala	Ser	Thr	Thr	Gly	Ser	Met	Ala	Ser	Asn	Asp	Gln	
	370					375					380					
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Glu	Asp	Glu	Thr	Met	Ser	Ile	Gly	Gly	Ile	Ala	Met	Ser	Ser	Gln	Thr	
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Ile	Thr	Ile	Gly	Val	Ser	Glu	Ile	Leu	Asn	Leu	Leu	Arg	Thr	Leu	Gly	
			405					410					415			
gaa	ggg	tgt	aga	ctt	tca	tac	atg	tac	agg	tgt	cag	gag	gca	ctg	gat	1296
Glu	Gly	Cys	Arg	Leu	Ser	Tyr	Met	Tyr	Arg	Cys	Gln	Glu	Ala	Leu	Asp	
			420					425					430			
acg	tat	atg	aaa	ctt	cca	cat	aag	cat	tat	aat	aca	gga	tgg	gtt	ctt	1344
Thr	Tyr	Met	Lys	Leu	Pro	His	Lys	His	Tyr	Asn	Thr	Gly	Trp	Val	Leu	
	435						440					445				
tcc	cag	gtc	ggg	aaa	gca	tac	ttt	gaa	cta	att	gac	tat	tta	gag	gct	1392
Ser	Gln	Val	Gly	Lys	Ala	Tyr	Phe	Glu	Leu	Ile	Asp	Tyr	Leu	Glu	Ala	
	450					455					460					
gaa	aag	gca	ttc	cgt	ctt	gcc	cgt	ctg	gct	tct	cct	tat	tgc	tta	gaa	1440
Glu	Lys	Ala	Phe	Arg	Leu	Ala	Arg	Leu	Ala	Ser	Pro	Tyr	Cys	Leu	Glu	
	465				470				475						480	
gga	atg	gat	ata	tac	tct	acg	gtc	ctc	tat	cat	ttg	aag	gaa	gac	atg	1488
Gly	Met	Asp	Ile	Tyr	Ser	Thr	Val	Leu	Tyr	His	Leu	Lys	Glu	Asp	Met	
			485					490					495			
aag	ctg	agt	tac	ttg	gct	cag	gaa	cta	ata	tca	acc	gat	cgc	tta	gct	1536
Lys	Leu	Ser	Tyr	Leu	Ala	Gln	Glu	Leu	Ile	Ser	Thr	Asp	Arg	Leu	Ala	
			500				505						510			
cct	caa	tct	tgg	tgt	gct	atg	gga	aat	tgc	tat	agc	ttg	caa	aag	gac	1584

Pro	Gln	Ser	Trp	Cys	Ala	Met	Gly	Asn	Cys	Tyr	Ser	Leu	Gln	Lys	Asp	
	515						520					525				
cat	gag	acc	gca	ctg	aag	aat	ttc	cta	cga	gct	gtt	caa	ctg	aat	cca	1632
His	Glu	Thr	Ala	Leu	Lys	Asn	Phe	Leu	Arg	Ala	Val	Gln	Leu	Asn	Pro	
	530					535					540					
aga	ttt	gca	tat	gca	cat	acc	tta	tgt	ggc	cac	gaa	tac	aca	act	ctt	1680
Arg	Phe	Ala	Tyr	Ala	His	Thr	Leu	Cys	Gly	His	Glu	Tyr	Thr	Thr	Leu	
	545				550					555					560	
gag	gat	ttt	gag	aac	gga	atg	aaa	agt	tac	caa	aac	gca	ctt	cgt	gta	1728
Glu	Asp	Phe	Glu	Asn	Gly	Met	Lys	Ser	Tyr	Gln	Asn	Ala	Leu	Arg	Val	
				565					570					575		
gat	aca	aga	cac	tac	aac	gca	tgg	tac	ggg	ctt	gga	atg	ata	tat	cta	1776
Asp	Thr	Arg	His	Tyr	Asn	Ala	Trp	Tyr	Gly	Leu	Gly	Met	Ile	Tyr	Leu	
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cgc	caa	gag	aag	tta	gag	ttc	tca	gag	cat	cac	ttc	aga	atg	gct	ttc	1824
Arg	Gln	Glu	Lys	Leu	Glu	Phe	Ser	Glu	His	His	Phe	Arg	Met	Ala	Phe	
	595					600						605				
cta	ata	aac	ccg	agt	tcc	tct	gtt	ata	atg	tct	tat	tta	ggg	aca	tct	1872
Leu	Ile	Asn	Pro	Ser	Ser	Ser	Val	Ile	Met	Ser	Tyr	Leu	Gly	Thr	Ser	
	610					615					620					
ttg	cat	gcc	ttg	aag	aga	agt	gag	gaa	gca	cta	gag	ata	atg	gag	caa	1920
Leu	His	Ala	Leu	Lys	Arg	Ser	Glu	Glu	Ala	Leu	Glu	Ile	Met	Glu	Gln	
	625				630					635				640		
gcc	ata	gta	gca	gat	aga	aaa	aac	cct	ctt	cca	atg	tac	cag	aaa	gct	1968
Ala	Ile	Val	Ala	Asp	Arg	Lys	Asn	Pro	Leu	Pro	Met	Tyr	Gln	Lys	Ala	
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aac	ata	ctt	gtc	tgc	tta	gaa	aga	tta	gat	gaa	gct	cta	gaa	gtt	ctt	2016
Asn	Ile	Leu	Val	Cys	Leu	Glu	Arg	Leu	Asp	Glu	Ala	Leu	Glu	Val	Leu	
		660						665					670			
gag	gag	ctc	aaa	gag	tat	gcg	cct	tca	gag	agc	agc	gtt	tac	gct	tta	2064
Glu	Glu	Leu	Lys	Glu	Tyr	Ala	Pro	Ser	Glu	Ser	Ser	Val	Tyr	Ala	Leu	
		675					680					685				
atg	ggc	agg	atc	tat	aag	cgg	cga	aac	atg	cac	gat	aaa	gcc	atg	ctt	2112
Met	Gly	Arg	Ile	Tyr	Lys	Arg	Arg	Asn	Met	His	Asp	Lys	Ala	Met	Leu	
	690					695					700					
cat	ttc	ggg	cta	gct	tta	gat	atg	aaa	ccg	cct	gca	act	gac	gtt	gct	2160
His	Phe	Gly	Leu	Ala	Leu	Asp	Met	Lys	Pro	Pro	Ala	Thr	Asp	Val	Ala	
	705				710					715					720	
gca	ata	aag	gct	gca	atg	gag	aaa	ttg	cat	gtt	cca	gat	gag	atc	gat	2208
Ala	Ile	Lys	Ala	Ala	Met	Glu	Lys	Leu	His	Val	Pro	Asp	Glu	Ile	Asp	
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gag	agc	ccg	tga													2220
Glu	Ser	Pro														

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Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe  
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Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Thr Ser Tyr Leu Gln Asn  
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Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala  
 50 55 60

Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu  
 65 70 75 80

Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu  
 85 90 95

Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys  
 100 105 110

Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu  
 115 120 125

Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu  
 130 135 140

Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln  
 145 150 155 160

Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu  
 165 170 175

Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser  
 180 185 190

Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser  
 195 200 205  
 Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser  
 210 215 220  
 Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala  
 225 230 235 240  
 Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn  
 245 250 255  
 Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu  
 260 265 270  
 Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile  
 275 280 285  
 Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu  
 290 295 300  
 Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser  
 305 310 315 320  
 Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Gly Ser Lys Leu Ser  
 325 330 335  
 Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala  
 340 345 350  
 Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser  
 355 360 365  
 Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln  
 370 375 380  
 Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr  
 385 390 395 400  
 Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly  
 405 410 415  
 Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp  
 420 425 430

Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu  
 435 440 445

Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala  
 450 455 460

Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu  
 465 470 475 480

Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met  
 485 490 495

Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala  
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Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp  
 515 520 525

His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro  
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Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Thr Leu  
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Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val  
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Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu  
 580 585 590

Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe  
 595 600 605

Leu Ile Asn Pro Ser Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser  
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Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln  
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Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala  
 645 650 655

Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu  
 660 665 670



Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu  
 675 680 685

Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu  
 690 695 700

His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala  
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16

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33

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36

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